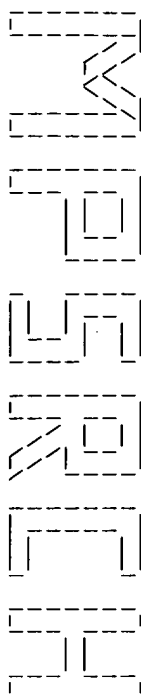


Thu Dec 16 12:41:39 1999

us38183-1-38183.pep

Page 1

US3A183-1-38183
MIDIDYKEFGATVILSELPDSDFSPYRLDLTAALYREALSEPHNSPHNLRALILICMELMTLAT
VGNVLEPASAERDLYVYSVYNTNGKLFROLFWHISCTLPEREYITELVSGWITPAIPYAPPAITL
SLPTEPTVYRRGSPSPRPTSPRRSPSPRRSSOSCEITRFDIELLODGPBELLVYLO
LALNDIDYKEFGATVILSELPDSDFSPYRLDLTAALYREALSEPHNSPHNLRALILICMELMT
LATVGNVLEPASAERDLYVYSVYNTNGKLFROLFWHISCTLPEREYITELVSGWITPAIPAPPA
PLISLPEPTVYRRGSPSPRPTSPRRSPSPRRSSOSCEITRFDIELLODGPBELLVYLO



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Mparch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 12:43:38 1999; Maspar time 17.14 Seconds
Tabular output not generated. 491.237 Million cell updates/sec

Title: >US38183-1-38183
Description: (1-396) from us38183-1-38183.pep
Perfect Score: 2977
Sequence: 1 MDIDPYKEFGATVELLSFLP.....RRRSQSPRRRSQSRSSOC 396
Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneeq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 33.376; Variance 170.298; scale 0.196
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1375	46.2	194	32	W50242	Hepatitis B virus pre
2	1375	46.2	212	32	W50250	Hepatitis B virus pre
3	1375	46.2	346	5	R27473	SL2/core protein.
4	1375	46.2	397	20	W03048	Plasmodium falciparum
5	1358	45.6	184	1	P80959	Hepatitis B virus sub
6	1358	45.6	193	32	W50251	Hepatitis B virus p21
7	1358	45.6	193	32	W50241	Hepatitis B virus p21
8	1353	45.4	183	20	W03044	Hepatitis B virus cor
9	1349	45.3	183	1	R05635	Hepatitis B antigen.
10	1349	45.3	183	5	P00041	Sequence of core anti
11	1338	44.9	196	5	P00004	Sequence of core anti
12	1336	44.9	196	8	R40808	Hepatitis B core / pV
13	1337	44.9	208	8	R40808	Hepatitis B core / pV
14	1334	44.8	183	8	R40805	Hepatitis B core prot
15	1334	44.8	183	8	R40805	Hepatitis B core prot
16	1334	44.8	183	13	R68868	Hepatitis B virus pol

17	1334	44.8	183	12	R62869	Hepatitis B virus cor
18	1333	44.8	198	8	R40807	Hepatitis B core / IL
19	1338	44.6	293	10	R55286	Pres1 full length cor
20	1335	44.5	183	13	R68866	Hepatitis B virus pol
21	1334	44.5	185	6	R30861	Hepatitis B core anti
22	1334	44.5	185	10	R55284	Deduced sequence of f
23	1324	44.5	185	6	R30780	Native HBcAg protein.
24	1324	44.5	185	6	R30780	Native HBcAg protein.
25	1335	44.5	214	1	P90702	Deduced amino acid se
26	1335	44.5	289	20	W03049	Plasmodium falciparum
27	1331	44.4	185	26	P30061	Core antigen of HBV.
28	1330	44.3	183	13	R68869	Hepatitis B virus pol
29	1337	44.2	185	6	R30781	Altered HBcAg protein
30	1317	44.2	185	6	R31026	Altered HBcAg protein
31	1314	44.1	183	13	R68867	Hepatitis B virus pol
32	1313	44.1	183	13	R68870	Hepatitis B virus pol
33	1311	44.0	185	6	R30784	Altered HBcAg protein
34	1311	44.0	185	6	R31029	Altered HBcAg protein
35	1311	44.0	185	6	R30865	Modified hepatitis B
36	1309	44.0	185	6	R30862	Hepatitis B core anti
37	1308	43.9	185	6	R31028	Altered HBcAg protein
38	1308	43.9	185	6	R30783	Altered HBcAg protein
39	1308	43.9	185	6	R30864	Modified hepatitis B
40	1303	43.8	214	1	P80961	HBV core antigen enco
41	1302	43.7	203	1	P82872	HBcAg/BetaGal fusion
42	1287	43.2	198	32	W50252	Hepatitis B virus pre
43	1263	42.4	183	17	R98878	Hepatitis B virus E a
44	1259	42.3	183	17	R98883	Hepatitis B virus E a
45	1258	42.3	183	17	R98884	Hepatitis B virus E a

ALIGNMENTS

RESULT 1
ID W50242: standard; Protein; 194 AA.
AC W50242:2 (first entry)
DE Hepatitis B virus precore p22 polypeptide Met-p22.
KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
KW hepatocyte; liver; Met-p22.
OS Hepatitis B virus.
OS Synthetic.
FH Key
FT Protein
FT 2.194
FT /Label- p22
PN W09809649-A1.
PD 12-MAR-1998.
PF 03-SEP-1997; U15500.
PR (GHEO) GEN HOSPITAL CORP.
PA (GHEO) GEN HOSPITAL CORP.
PI Melegari M, Scaglioni PP, Wands JR;
DR WPI: 98-193325/17.
PT DNA encoding proteins which can be incorporated with wild type
PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
PT inhibition of viral replication, especially hepatitis B virus
PS Claim 11; Page 40; 60pp; English.
CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
CC protein with an added N-terminal Met residue. p22 is produced by
CC elimination of the 19-amino acid leader peptide from the 25 kDa
CC full-length HBV precore protein (see W50250). Evidence is provided
CC that HBV replication is inhibited in the presence of high levels of
CC HBV precore or precore-related proteins. These proteins can be
CC incorporated into HBV nucleocapsids along with the p21 core protein
CC (see W50251), which is the usual nucleocapsid component, and
CC thereby render the nucleocapsids deficient in encapsidating HBV
CC pregenomic RNA. Thus, over-expression of the precore proteins, or
CC certain variants of them, leads to transdominant inhibition of HBV
CC replication. Suitable inhibitory proteins include p25 (see W50250),
CC p22, Met-p22, p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
CC (see W50238). Heterologous peptides (see W50244-49) may be
CC inserted into the p22 and Met-p22 polypeptides. The inhibitory
CC proteins can be produced by recombinant methods using claimed
CC expression vectors and host cells. They can be provided exogenously

CC to the target cells for use in inhibiting HBV replication.
 CC Alternatively, a nucleic acid construct that directs overexpression
 CC of an inhibitory protein in target cells is used for the gene
 CC therapy of HBV infection.
 SO Sequence 194 AA;

Query Match 46.2%; Score 1375; DB 32; Length 194;
 Best Local Similarity 99.5%; Pred. No. 1,53e-101;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 gmdidpykefatavellsfpsdfpsvrdldtasalyrealsepncphthalrqa1 70
 :|||||
 QY 213 SMDIDPKEGATVELLSEFLPSDFPSVRDLDTASALYREALSEPHCSHHTALRQAI 272
 273 LCWGEIMLTATWGVNLEDPASRDLVSVYNTNMGLFROLMFHISCLFGRFETVLEYL 332
 Db 131 vsfgvwtirppayrppnapllstlpettvrrrgsprrrrrrrrrsgsprrrrrsgsr 190
 :|||||
 QY 333 VSEGVWIRTPAPRPPNAPILSTLPETTVARRKGRSPRRRTPSPRRRSQSR 392
 Db 191 esgc 194
 :||||
 QY 393 ESQC 396

RESULT 2
 ID W50250 standard; Protein; 212 AA.
 AC W50250;

DT 28-SEP-1998 (first entry)
 DE Hepatitis B virus precore p25 polypeptide.
 KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
 KM Hepatocyte; liver; p25 protein.
 OS Hepatitis B virus.
 PN W09809649-A1.
 PD 12-MAR-1998.
 PE 03-SEP-1997; U15500.
 PR 03-SEP-1996; US-025370.
 PA (GEHO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR;
 DR WPI: 98-193325/17.
 PT DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus
 PT Claim 15, Page 35; 60pp; English.
 CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)
 CC protein that is encoded by the full-length HBV precore gene.
 CC Evidence is provided that HBV replication is inhibited in the
 CC presence of high levels of HBV precore or precore-related proteins.
 CC These proteins can be incorporated into HBV nucleocapsids along
 CC with the p21 core protein (see W50251), which is the usual
 CC nucleocapsid component, and thereby render the nucleocapsids
 CC deficient in encapsidating HBV pregenomic RNA. Thus, over-
 CC expression of the precore proteins, or certain variants of them,
 CC leads to transdominant inhibition of HBV replication. Suitable
 CC inhibitory proteins include p25, p22 (see W50241), Met-p22 (see
 CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
 CC (see W50238). The inhibitory proteins can be produced by
 CC recombinant methods using claimed expression vectors and host
 CC cells. They can be provided exogenously to the target cells for
 CC use in inhibiting HBV replication. Alternatively, a nucleic acid
 CC construct that directs overexpression of an inhibitory protein in
 CC target cells is used for the gene therapy of HBV infection.
 SO Sequence 212 AA;

Query Match 46.2%; Score 1375; DB 32; Length 212;
 Best Local Similarity 99.5%; Pred. No. 1,53e-101;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 gmdidpykefatavellsfpsdfpsvrdldtasalyrealsepncphthalrqa1 88
 :|||||
 QY 213 SMDIDPKEGATVELLSEFLPSDFPSVRDLDTASALYREALSEPHCSHHTALRQAI 272

Db 89 lcwgeimltatwgvnledpasrdlvsvyntnmglkfrrllwfhiscslfgrtvey1 148
 :|||||
 QY 273 LCWGEIMLTATWGVNLEDPASRDLVSVYNTNMGLFROLMFHISCLFGRFETVLEYL 332
 Db 149 vsfgvwtirppayrppnapllstlpettvrrrgsprrrrrrrrrsgsprrrrrsgsr 208
 :|||||
 QY 333 VSEGVWIRTPAPRPPNAPILSTLPETTVARRKGRSPRRRTPSPRRRSQSR 392
 Db 209 esgc 212
 :||||
 QY 393 ESQC 396

RESULT 3
 ID R27473 standard; Protein; 346 AA.
 AC R27473;

DT 24-FEB-1993 (first entry)
 DE S12/core protein.
 KW Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
 KW vaccinia virus; 13L; promoter; NYVAC; recombinant; HBV L;
 KW large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;
 KW S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;
 KW deletion loci; recipient loci.
 OS Synthetic.
 FH Key
 FT region Location/Qualifiers
 FT 1..108 /label S1
 FT region 109..163 /label= S2
 FT 164..346 /label= S2
 FT region /label= Core
 PN W09215672-A.
 PD 17-SEP-1992.
 PE 09-MAR-1992; U01906.
 PR 07-MAR-1991; US-666056.
 PR 11-JUN-1991; US-713967.
 PR 06-MAR-1992; US-847951.
 PA (VIRRO-) VIROGENETICS CORP.
 PI Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GP,
 PI Lambach KJ, Norton ER, Paoletti E, Perkins ME, Pincus SE,
 PI Riviere M, Tarantola J, Taylor J;
 DR WPI: 92-331718/40.
 DR N-PSDB: Q29105.
 PT Vaccine comprises recombinant, attenuated pox-virus - use for
 PT vaccinating against viral infections such as rabies, hepatitis B,
 PT HIV, HSV, EBV, CMV, mumps etc.
 PS Disclosure: Fig 13; 456pp; English.

CC The sequence given is encoded by an expression cassette which
 CC comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/
 CC core) which is precisely linked to the 13L promoter derived from
 CC vaccinia virus. This DNA sequence was linked to the S1 and S2
 CC sequences and this fragment was used in the construction of a NYVAC
 CC recombinant expressing the HBV gene. Other HBV genes were also used
 CC in the construction. These were HBV M protein (small pre-S antigen,
 CC spsAg) and HBV L (large pre-S antigen, lpsAg). Each of these gene
 CC sequences were inserted individually into three different sites of
 CC NYVAC separated by from each other by large regions of vaccinia DNA
 CC containing essential genes. NYVAC is a Copenhagen vaccine strain of
 CC vaccinia virus which has been modified by deletion of six non-essential
 CC regions of the genome encoding known or potential virulence factors.
 CC The deletion loci were engineered as recipient loci for the insertion
 CC of foreign genes. The spacing of the three inserted sequences ensured
 CC that any recombination that did occur would lead to disruption of the
 CC vaccinia genome and would cause unviable vaccinia virus. See also
 CC Q35501-864.
 SO Sequence 346 AA;

Query Match 46.2%; Score 1375; DB 5; Length 346;
 Best Local Similarity 99.5%; Pred. No. 1,53e-101;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 163 nmddidpykefatavellsfpsdfpsvrdldtasalyrealsepncphthalrqa1 222

[illegible]

Query	Match	Similarity	Score	DB	Length	Pos	Indels	Gaps
Matches 181; Conservative	181; Conservative	2; Pident. 5.32e-100;	1;	Indels 0;	Gaps 0;			
Query Match	45.6%;	Score 1359;	DB 32;	Length 193;				
Best Local Similarity	98.4%;	Pident. 5.32e-100;	1;	Indels 0;	Gaps 0;			
Db	10 gmdldpykefatvellsffpsdfpsvrdlthasalyreallespcshptalrqai	69						
Qy	213 SMDIDPYKEFATVYELSLFSDPFPYVRDLDTASLYKLEALESPHRCSPHTALRQAI	272						
Db	70 lwcgelmrlatvynvlnedpasrdilvsvydtngmlkfrqlwfmalsclffgretvleyl	129						
Qy	273 LCMGELMLRLAVMGVNIEDPASRDILVSVYNTNGMLFQRLMWHISCLFGRVTEIYL	332						
Db	130 vsfgwiltppayrpnapilsltpettvrrrrsprrrrrsprrrrrsprrrrrsgsr	169						
Qy	333 VSFGWIRTPPAYRPNPAPILSLTPEITVYRRRGRSPRRRTPSPRRRRSQSPRRRRSQSR	392						
Db	190 esgc 193							
Qy	393 ESQC 396							
RESULT	8							
ID	M03044 standard; protein; 183 AA.							
DT	11-APR-1997 (first entry)							
DE	Hepatitis B virus core protein.							
KM	Hepadnavirus; HBV; woodchuck hepatitis virus; hepatitis delta virus;							
KW	ground squirrel hepatitis B virus; duck hepatitis B virus;							
OS	core protein; replication; antiviral; gene therapy.							
FT	Hepatitis B virus.							
FT	Key							
FT	Location/Qualifiers							
FT	misc_difference 71..180							
FT	/note- "C-terminus of core protein is at any amino							
FT	acid position between 71-180 in mutant							
FT	polypeptides of the invention (Claim 23)"							
FT	81..180							
FT	/note- "C-terminus of core protein is at any amino							
FT	acid position between 81 and 180 in mutant							
FT	polypeptides of the invention (Claim 5)"							
FT	171..180							
FT	/note- "C-terminus of core protein is at any amino							
FT	acid position between 171 and 180 in mutant							
FT	polypeptides of the invention (Claim 6)"							
FT	174..180							
FT	/note- "C-terminus of core protein is at any amino							
FT	acid position between 174 and 180 in mutant							
FT	polypeptides of the invention (Claim 26)"							
FT	178							
FT	/note- "C-terminus of core protein is at amino acid							
FT	position 178 in mutant polypeptides of the							
FT	invention (Claim 7)"							

FT misc_difference 178
 /note- "C-terminus of core protein is at amino acid
 position 178 in mutant polypeptides of the
 invention (Claim 7)"
 FT misc_difference 172..183
 /note- "amino acid residues 172-183, pref. 174-180,
 are deleted from the core protein in mutant
 polypeptides of the invention"
 FT WO9700698-A1.
 PN 09-JAN-1997.
 PD 20-JUN-1996: U10602.
 PR 20-JUN-1995: US-017814.
 PA (GENO.) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR.
 DR N-PSDB: T49594.
 PT New method for inhibiting the replication of hepadnaviruses -
 PT comprises introducing a mutant polypeptide with a mutated core
 PT protein or corresponding nucleic acid, for treating, e.g. hepatitis
 PT B
 PS Claim 5: Page 55-56: 83pp: English.
 CC Alteration of the C-terminus of the core protein (W09044) of
 CC hepatitis B virus (HBV) or other hepadnavirus creates a mutant
 CC polypeptide capable of reducing replication of the wild-type virus
 CC by a dominant negative mechanism. The inhibitory effect is
 CC species-specific and is achieved by deletion of a few C-terminal
 CC amino acids from the core protein, and/or by joining the core
 CC protein to a hepadnavirus surface protein (see also W09045),
 CC creating a core-surface fusion. Such mutant polypeptides (see
 CC also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
 CC infection.
 SQ Sequence 183 AA:

Query Match 45.4%; Score 1353; DB 20; Length 183;
 Best Local Similarity 98.9%; Pred. No. 1.04e-99;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 mdidpykefagatvellsfipdsffpsvrdlldtaaalrydalespncshphltalrgail 60
 |||
 Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPENCSPHHTLRQAIL 60
 |||
 Db 61 cswgelmrlatwgvnledpsardlvsvytnmglkrqlmfrhiscrtferevteylyv 120
 |||
 Qy 61 CWSGELMLTATWGVNLEDPSARDLVSVYTNMGLKRFQLMFRHISCTFERETVEYLYV 120
 |||
 Db 121 sfgywltppayrpnapilslpeltvrrrgsrprtrrrpsrrrrsgsrrrrsgare 180
 |||
 Qy 121 SFGWLTTPPAYRPNAPILSLPETVRRRGSRPRTRRRSPRRRSQSPRRRSQSRE 180
 |||
 Db 181 sqc 183
 |||
 Qy 181 SQC 183

RESULT 9
 ID R05635 standard; protein; 183 AA.
 AC R05635;
 DT 30-OCT-1990 (first entry)
 DE Hepatitis B antigen.
 KM Hepatitis B virus; vaccine; HBV; ds.
 OS Synthetic.
 PN EP-374869-A.
 PD 27-JUN-1990.
 PF 1-JAN-1989: 123526.
 PR 22-DEC-1978: GB-049907.
 PR 22-DEC-1978: GB-050039.
 PR 01-NOV-1979: GB-037910.
 PA (BIOJ) Biogen Inc.
 PI Murray K, Schaller HE;
 DR N-PSDB: 004799
 DR N-PSDB: 004799
 PT Recombinant DNA encoding Hepatitis B virus polypeptide antigens -
 PT used in detection of infection and in vaccine prodn.

PS Disclosure; 4pp: English.
 CC Polypeptide fragments encoded by the DNA sequence are antigenic for
 CC HBV and may be used as a vaccine or in detection. Peptides may be
 CC cultured in a suitable bacterial host such as E.coli.
 CC Fragments of the sequence are also claimed as being antigenically
 CC useful.
 SQ Sequence 183 AA:

Query Match 45.3%; Score 1349; DB 1; Length 183;
 Best Local Similarity 96.7%; Pred. No. 2.24e-99;
 Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdidpykefagatvellsfipdsffpsvrdlldtaaalrydalespncshphltalrgail 60
 |||
 Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPENCSPHHTLRQAIL 60
 |||
 Db 61 cswgelmrlatwgvnledpsardlvsvytnmglkrqlmfrhiscrtferevteylyv 120
 |||
 Qy 61 CWSGELMLTATWGVNLEDPSARDLVSVYTNMGLKRFQLMFRHISCTFERETVEYLYV 120
 |||
 Db 121 sfgywltppayrpnapilslpeltvrrrgsrprtrrrpsrrrrsgsrrrrsgare 180
 |||
 Qy 121 SFGWLTTPPAYRPNAPILSLPETVRRRGSRPRTRRRSPRRRSQSPRRRSQSRE 180
 |||
 Db 181 sqc 183
 |||
 Qy 181 SQC 183

RESULT 10
 ID P00041 standard; protein; 183 AA.
 AC P00041;
 DT 14-OCT-1992 (first entry)
 DE Sequence of core antigen.
 KM Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
 OS Hepatitis B virus.
 PN EP-13828-A.
 PD 06-AUG-1980.
 PF 21-DEC-1979: 303017.
 PF 22-DEC-1978: GB-049907.
 PR 27-DEC-1978: GB-050039.
 PR 01-NOV-1979: GB-037910.
 PA (BIOJ) BIOGEN NV.
 PI Murray K, Schaller HE;
 DR N-PSDB: N00003.
 DR N-PSDB: N00003.
 PT Recombinant DNA coding for polypeptide - have specificity of
 PT hepatitis B viral antigens in detection or antibody stimulation
 PS Example: Figs 3-4; 43pp: English.
 CC Human serum from a single HBeAg positive, HBeAg positive donor
 CC (serotype adyM) was used to prep. a DNA-contg. pellet which was
 CC labelled with 3H or 32P as described by P. M. Kaplan et al (1973).
 CC The labelled DNA was then extracted with phenol from the resulting
 CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
 CC It was then cloned in plasmid pBR322 which was used to transform E.
 CC coli. Micro-organisms prepd. by the processes are deposited at the
 CC HBV-Kpn I dC: Tetr Amps HBV+.

Query Match 45.3%; Score 1349; DB 5; Length 183;
 Best Local Similarity 96.7%; Pred. No. 2.24e-99;
 Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdidpykefagatvellsfipdsffpsvrdlldtaaalrydalespncshphltalrgail 60
 |||
 Qy 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPENCSPHHTLRQAIL 60
 |||
 Db 61 cswgelmrlatwgvnledpsardlvsvytnmglkrqlmfrhiscrtferevteylyv 120
 |||
 Qy 61 CWSGELMLTATWGVNLEDPSARDLVSVYTNMGLKRFQLMFRHISCTFERETVEYLYV 120
 |||
 Db 121 sfgywltppayrpnapilslpeltvrrrgsrprtrrrpsrrrrsgsrrrrsgare 180
 |||


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QY 212 LMSDIDPYKEFGATVELLSLPSDFPSVRDLDTASALYREALSEPHCHSPHHTALRQA 271
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 84 Cwgelmlatwvgsnledpasrelvsvyvnmgikrlqlwfhiscitfgretvley 143
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 ILWGELMTLATWGVNLEDPASRDVSVYVNTNMGKLFROLFWHISCLTFRGRTVLEY 331
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 lvsfgwlrtpayrppnapilsltpetvvrirgsprrrrrrrrrrrrrrrrrrrrrr 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 332 LVSGFWIRTPPAYRPPNAPILSLTPEITVVRRRGRSPRRRTSPRRRRRSGSPRRRSQS 391
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 204 resgc 208
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 392 RESQC 396

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RESULT 14
ID P40311 standard; Protein: 183 AA.
AC P40311;
DT 18-AUG-1992 (first entry)
DE Hepatitis virus core antigen.
KM HBcAg; vaccine; diagnosis; HBV infection.
OS Hepatitis b virus.
PN J59074985-A.
PD 27-APR-1984.
PF 19-OCT-1982; 183432.
PR 19-OCT-1982; JP-183432.
PA (TAKE ) TAKEDA CHEMICAL IND KK.
DR WPI: 84-143231/23.
PT DNA used in prevention of infections by hepatitis virus B -
PT comprises structural gene of hepatitis virus adr B surface antigen
PT coding gene and at least 1 virus core antigen structural gene.
PS Disclosure; Fig 3; 13p; Japanese.
CC The sequence is that of hepatitis virus core antigen (HBcAg). It
CC can be used as a vaccine for the prevention of infections by
CC hepatitis B virus (HBV) and also in the diagnosis of early stages
CC of HBV infection. See also P40310.
SQ Sequence 183 AA;

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Query Match 44.88; Score 1334; DB 4; Length 183;
Best Local Similarity 95.68; Pred. No. 3.99e-98;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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```

DB 1 mdldpykefgasvellsfjpsdfpsirdlldtasalyrealsepchsphtalrqail 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1 MDIDPYKEFGATVELLSLPSDFPSVRDLDTASALYREALSEPHCHSPHHTALRQA 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 Cwgelmlatwvgsnledpasrelvsvyvnmgikrlqlwfhiscitfgretvley 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKLFROLFWHISCLTFRGRTVLEY 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 sfvgwlrtpayrppnapilsltpetvvrirgsprrrrrrrrrrrrrrrrrrrrrr 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 SFGVWIRTPPAYRPPNAPILSLTPEITVVRRRGRSPRRRTSPRRRRRSGSPRRRSQS 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 sgc 183
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 SOC 183

```

```

RESULT 15
ID R40805 standard; Protein: 183 AA.
AC R40805;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core protein.
KM Hepatitis B: core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Hepatitis B virus.
PN J05192170-A.
PD 03-AUG-1993.
PF 24-SEP-1991; 243800.
PR 24-SEP-1991; JP-243800.
PA (NISW ) NISSHIN OIL MILLS LTD.
DR WPI: 93-277479/35.

```

```

DR N-PSDB; Q47735
PT Recombinant plasmid for high immunogenicity virus - contains
PT recombinant haemagglutinin gene, hepatitis B core gene of vaccinia
PT virus and exotic genes
PS Disclosure; Fig 6; 12p; Japanese.
CC The hepatitis B core gene is recombined with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.
SQ Sequence 183 AA;

```

```

Query Match 44.88; Score 1334; DB 8; Length 183;
Best Local Similarity 95.68; Pred. No. 3.99e-98;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

DB 1 mdldpykefgasvellsfjpsdfpsirdlldtasalyrealsepchsphtalrqail 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1 MDIDPYKEFGATVELLSLPSDFPSVRDLDTASALYREALSEPHCHSPHHTALRQA 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 Cwgelmlatwvgsnledpasrelvsvyvnmgikrlqlwfhiscitfgretvley 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 CWGELMTLATWGVNLEDPASRDVSVYVNTNMGKLFROLFWHISCLTFRGRTVLEY 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 sfvgwlrtpayrppnapilsltpetvvrirgsprrrrrrrrrrrrrrrrrrrrrr 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 SFGVWIRTPPAYRPPNAPILSLTPEITVVRRRGRSPRRRTSPRRRRRSGSPRRRSQS 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 sgc 183
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 SOC 183

```

```

Search completed: Thu Dec 16 12:47:00 1999
Job time : 202 secs.

```

NW5EQLF1
***** (TW)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 12:47:19 1999; Maspar time 18.46 Seconds
Tabular output not generated. 859.536 Million cell updates/sec

Title: >US38183-1-38183
Description: (1-396) from US38183-1-38183.pep
Perfect Score: 2977
Sequence: 1 MDIDPYKEGATVELLSFLP.....RRRRSQSPRRRSQSRSSOC 396

Scoring table:
PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p160
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 46.943; Variance 114.459; scale 0.410

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1375	46.2	212	1	NKVLAH e antigen precursor / 1.95e-206	
2	1374	46.2	212	2	S53211 e antigen precursor / 2.85e-206	
3	1374	46.2	212	2	S53204 e antigen precursor / 2.85e-206	
4	1373	46.1	183	2	S53207 core antigen - hepati / 4.24e-206	
5	1373	46.1	212	2	S20750 e antigen precursor / 4.24e-206	
6	1370	46.0	183	2	S53270 core antigen - hepati / 1.39e-205	
7	1370	46.0	212	2	S53216 e antigen precursor / 1.39e-205	
8	1370	46.0	212	2	S53272 e antigen precursor / 1.39e-205	
9	1369	46.0	212	2	S53163 e antigen precursor / 2.07e-205	
10	1369	46.0	212	2	S20746 e antigen precursor / 2.07e-205	
11	1368	46.0	212	2	S53225 e antigen precursor / 2.07e-205	
12	1368	46.0	212	2	S53198 e antigen precursor / 3.08e-205	
13	1366	45.9	212	2	S53223 e antigen precursor / 6.81e-205	
14	1366	45.9	212	2	S53274 e antigen precursor / 6.81e-205	
15	1364	45.8	183	2	S53169 core antigen - hepati / 1.51e-204	
16	1363	45.8	183	2	S53247 core antigen - hepati / 2.24e-204	
17	1363	45.8	212	2	S53202 e antigen precursor / 2.24e-204	
18	1363	45.8	212	2	S53159 e antigen precursor / 2.24e-204	
19	1363	45.8	212	2	S53200 e antigen precursor / 2.24e-204	
20	1362	45.8	212	2	S53251 e antigen precursor / 3.33e-204	
21	1360	45.7	212	2	S53204 e antigen precursor / 7.37e-204	
22	1360	45.7	212	2	S53227 e antigen precursor / 7.37e-204	
23	1358	45.6	211	1	NKVLAI e antigen precursor / 1.63e-203	

24	1359	45.6	212	2	S53253 e antigen precursor / 1.10e-203
25	1357	45.6	212	2	S53281 e antigen precursor / 2.42e-203
26	1355	45.5	212	1	NKVLBH e antigen precursor / 5.35e-203
27	1355	45.5	212	2	S53242 e antigen precursor / 5.35e-203
28	1351	45.4	183	2	S53129 core antigen - hepati / 2.62e-202
29	1351	45.4	212	2	S53240 e antigen precursor / 2.62e-202
30	1349	45.3	183	1	NKVLAI core antigen - hepati / 5.78e-202
31	1349	45.3	183	2	S53181 core antigen - hepati / 5.78e-202
32	1348	45.3	183	2	S53232 core antigen - hepati / 8.60e-202
33	1348	45.3	183	2	S53260 core antigen - hepati / 8.60e-202
34	1345	45.2	183	2	S53152 core antigen - hepati / 2.83e-201
35	1343	45.1	183	2	S53214 core antigen - hepati / 6.25e-201
36	1342	45.1	183	2	S53140 core antigen - hepati / 9.28e-201
37	1344	45.1	212	2	S53229 e antigen precursor / 4.20e-201
38	1341	45.0	183	2	S53267 core antigen - hepati / 1.38e-200
39	1341	45.0	183	2	S53189 core antigen - hepati / 1.38e-200
40	1339	45.0	183	2	S53137 core antigen - hepati / 3.05e-200
41	1341	45.0	212	2	S53238 e antigen precursor / 1.38e-200
42	1340	45.0	212	2	S53257 e antigen precursor / 2.05e-200
43	1339	45.0	212	2	S23651 e antigen precursor / 3.05e-200
44	1338	44.9	212	2	S53236 e antigen precursor / 4.54e-200
45	1337	44.9	212	1	NKVLJ2 e antigen precursor / 6.75e-200

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE NKVLAH #type complete
e antigen precursor / core antigen - hepatitis B virus
(subtype ayw4, isolate hb321 and others)
ALTERNATE_NAMES HBe antigen precursor / HBe antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus; HBV
#variety subtype ayw4, isolate hb321; isolate patient Ferracuti/83;
isolate patient Castag/83; isolate patient Sanna/84;
isolate patient Licheri-1/85; isolate patient Flore-1/86;
isolate patient Licheri/83

DATE 18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change 10-Oct-1997
ACCESSIONS S47405; S53191; S53209; S53234; S53264; S53249; S53262;
S53277; A03711

REFERENCE S47404
#authors Plucienniczak, A.
#submission Submitted to the EMBL Data Library, August 1994
#description Molecular cloning and sequencing of two complete genomes of
polish isolates of human hepatitis B virus.

#accession S47405
#molecule_type DNA
#residues 1-212 #label PUJ
#cross-references EMBL:235716; NID:9527435; PID:9527437
#experimental_source subtype ayw4, isolate hb321

REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission Submitted to the EMBL Data Library, March 1995
#description

#accession S53191
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85283; NID:9736088; PID:9736090
#experimental_source isolate patient Ferracuti/83

#accession S53209
#molecule_type DNA
#residues 1-212 #label LA2
#cross-references EMBL:X85290; NID:9736114; PID:9736116
#experimental_source isolate patient Castag/83

#accession S53234
#molecule_type DNA
#residues 1-212 #label LA3
#cross-references EMBL:X85300; NID:9736150; PID:9736152
#experimental_source isolate patient Sanna/84

#accession S53364
#molecule_type DNA
#residues 1-212 #label LA4
#cross-references EMBL:X85313; NID:9736194; PID:9736196

##experimental_source isolate patient Licheri-1'85
#accession S53249
##molecule_type DNA
##residues 1-212 ##label LA5
##cross-references EMBL:X85306; NID:g736172; PID:g736174
##experimental_source isolate patient Flore-1'86
#accession S53262
##molecule_type DNA
##residues 1-212 ##label LA6
##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
#accession S53277
##molecule_type DNA
##residues 30-212 ##label LA7
##cross-references EMBL:X85317; NID:g736211; PID:g736214
##experimental_source patient Giordo-2'86
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be processed

REFERENCE A93214
#authors Galibert, F.; Mandart, E.; Filoussi, F.; Tiollais, P.;
#journal Nature (1979) 281:646-650
#title Nucleotide sequence of the hepatitis B virus genome (subtype
ayw) in F. coli.
#cross-references M01D:81012091
#accession A03711
##molecule_type DNA
##residues 1-212 ##label GAL
##cross-references GB:J02203; NID:g329640; PID:g329642
##experimental_source subtype ayw

GENETICS C
#gene #superfamily hepatitis B virus core antigen
#alternative initiators; core protein

CLASSIFICATION
KEYWORDS
FEATURE 1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24350 #checksum 782

Query Match 46.2%; Score 1375; DB 1; Length 212;
Best Local Similarity 99.5%; Pred. No. 1.92e-206;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFSDFFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
QY 213 SMDIDPKFEGATVELLSFSDFFPSVRDLDTASALYREALSPHCSPHHTALRQAI 272

Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 148
QY 273 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 332

Db 149 VSEGVWIRTPAPYPPNAPILSTPETTVRRGRSPRRRPPSPRRRSQSPRRRSQSR 208
QY 333 VSEGVWIRTPAPYPPNAPILSTPETTVRRGRSPRRRPPSPRRRSQSPRRRSQSR 392

Db 209 ESOC 212
QY 393 ESOC 396

RESULT 2
ENTRY S53211 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Castag-1'85 and others)
ALTERNATE_NAMES HBC antigen; HBe antigen precursor / HBC antigen; pre-C/C
antigen
CONTAINS core antigen; e antigen
ORGANISM #formal name hepatitis B virus, HBV
#isolate patient Castag-1'85; isolate patient Ferracuti-1'89
#variety 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

08-Sep-1997
#accessions S53211; S53197
#authors Lai, M.E.; Mazzeoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53211
##molecule_type DNA
##residues 1-212 ##label LA1
##cross-references EMBL:X85291; NID:g736117; PID:g736119
##experimental_source isolate patient Castag-1'85
#accession S53197
##molecule_type DNA
##residues 30-212 ##label LAN
##cross-references EMBL:X85284; NID:g736095; PID:g736098
##experimental_source isolate patient Ferracuti-1'89
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS C
#gene #superfamily hepatitis B virus core antigen
#alternative initiators; core protein

CLASSIFICATION
KEYWORDS
FEATURE 1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24336 #checksum 746

Query Match 46.2%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 2.85e-206;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFSDFFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
QY 213 SMDIDPKFEGATVELLSFSDFFPSVRDLDTASALYREALSPHCSPHHTALRQAI 272

Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 148
QY 273 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 332

Db 149 VSEGVWIRTPAPYPPNAPILSTPETTVRRGRSPRRRPPSPRRRSQSPRRRSQSR 208
QY 333 VSEGVWIRTPAPYPPNAPILSTPETTVRRGRSPRRRPPSPRRRSQSPRRRSQSR 392

Db 209 ESOC 212
QY 393 ESOC 396

RESULT 3
ENTRY S32204 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C1000)
ALTERNATE_NAMES HBe antigen precursor / HBe antigen; pre-C/C antigen
core antigen; e antigen
CONTAINS core antigen; e antigen
ORGANISM #formal name hepatitis B virus, HBV
#subline ayw, patient C1000
#variety 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997

ACCESSIONS S32204
REFERENCE S32202
#authors Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.;
Gerok, W.; Rasenack, J.
#submission submitted to the EMBL Data Library, March 1993
#description Identification and sequence analysis of hepatitis B virus DNA
in immunological negative infection.
#accession S32204
##molecule_type DNA
##residues 1-212 ##label PRE
##cross-references EMBL:X72702; NID:g288927; PID:g288930
##experimental_source subtype ayw, patient C1000
#note due to a stop codon between the alternative initiators

the e antigen precursor cannot be produced

GENETICS

CLASSIFICATION C
#gene #superfamily hepatitis B virus core antigen
KEYWORDS core protein
FEATURE

1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #product e antigen #status predicted #label ENG\
#domain carboxyl-terminal propeptide #link ENG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24336 #checksum 770

Query Match 46.1%; Score 1374; DB 2; Length 212;

Best Local Similarity 98.9%; Pred. No. 2,456-206;

Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALROAI 88

QY 213 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALROAI 272

Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMHISCLTGRETVIELY 148

QY 273 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMHISCLTGRETVIELY 332

Db 149 VSEGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 208

QY 333 VSEGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 392

Db 209 ESOC 212

QY 393 ESOC 396

RESULT

ENTRY 4

TITLE S53207 #type complete

ALTERNATE_NAMES core antigen - hepatitis B virus (isolate patient

CONTAINS HBC antigen

ORGANISM #formal_name hepatitis B virus, HBV

DATE #variety isolate patient Castaa-2'87

08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

ACCESSIONS S53207

REFERENCE S53112

#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

#submission submitted to the EMBL Data Library, March 1995

#accession S53207

##molecule_type DNA

##residues 1-183 ##label LAI

##cross-references EMBL:X85289; NID:g736110; PID:g736113

##experimental_source isolate patient Castaa-2'87

##note due to a stop codon between the alternative initiators

the e antigen precursor cannot be produced

GENETICS

CLASSIFICATION C

#gene #superfamily hepatitis B virus core antigen

KEYWORDS core protein

SUMMARY #length 183 #molecular-weight 21102 #checksum 2165

Query Match 46.1%; Score 1373; DB 2; Length 183;

Best Local Similarity 99.5%; Pred. No. 4,246-206;

Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALROAI 60

QY 1 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALROAI 60

Db 61 CMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMHISCLTGRETVIELY 120

QY 61 CMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMHISCLTGRETVIELY 120

Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 180

QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 180

Db 181 SOC 183

QY 181 SOC 183

RESULT

ENTRY 5

TITLE S20750 #type complete

ALTERNATE_NAMES e antigen precursor / core antigen - hepatitis B virus

CONTAINS (subtype ayw, patient CI)

ORGANISM HBe antigen precursor / HBe antigen; pre-C/C antigen

DATE #variety core antigen; e antigen

08-Sep-1997 #formal_name hepatitis B virus, HBV

20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change

ACCESSIONS S20750

REFERENCE S20745

#authors Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.;

Porru, A.

#submission submitted to the EMBL Data Library, March 1992

#description Sequence analysis of HBV genomes isolated from patients with

HBeAg negative chronic liver disease.

#accession S20750

##molecule_type DNA

##residues 1-212 ##label LAI

##cross-references EMBL:X65258; NID:g59434; PID:g59436

##experimental_source subtype ayw, patient CI

GENETICS

CLASSIFICATION C

#gene #superfamily hepatitis B virus core antigen

KEYWORDS alternative initiators; core protein

FEATURE

1-29

30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #product e antigen #status predicted #label ENG\
#domain carboxyl-terminal propeptide #link ENG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 147

Query Match 46.1%; Score 1373; DB 2; Length 212;

Best Local Similarity 98.9%; Pred. No. 4,246-206;

Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALROAI 88

QY 213 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCHSPHHTALROAI 272

Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMHISCLTGRETVIELY 148

QY 273 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMHISCLTGRETVIELY 332

Db 149 VAFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 208

QY 333 VAFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 392

Db 209 ESOC 212

QY 393 ESOC 396

Db 209 ESOC 212

QY 393 ESOC 396

RESULT

ENTRY 6

TITLE S53270 #type complete

ALTERNATE_NAMES core antigen - hepatitis B virus (isolate patient

CONTAINS Licheri-2'87)

ORGANISM HBC antigen

DATE #variety core antigen

08-Jul-1995 #formal_name hepatitis B virus, HBV

isolate patient Licheri-2'87

03-Aug-1995 #sequence_revision 03-Aug-1995 #text_change

```

ACCESSIONS      08-Sep-1997
REFERENCE       S53270
#authors       Lai, M.E.; Mazzioleni, A.P.; Porru, A.; Balestrieri, A.
#submission    Submitted to the EMBL Data Library, March 1995
#accession     S53270
#residues     1-183
#molecule_type DNA
#cross-references EMBL:X85314; NID:q736201; PID:q736204
#experimental_source isolate patient Licheri-2/87
#note          due to a stop codon between the alternative initiators
               the e antigen precursor cannot be produced

GENETICS
CLASSIFICATION C
KEYWORDS       #superfamily 'hepatitis B virus core antigen
               core protein
SUMMARY        #length 183 #molecular-weight 21102 #checksum 2199

Query Match      46.0%; Score 1370; DB 2; Length 183;
Best Local Similarity 98.4%; Pred. No. 1.39e-205;
Matches 180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKEFGATVELLSLPDSFPSPRDLDITASALYRDALSPHCSPHHALRAIL 60
Oy 1 MDIDPKKEFGATVELLSLPDSFPSPRDLDITASALYRELSPHCSPHHALRAIL 60
||:|||||
61 CWMGLMTLATVWGVNLDPASRDLVSVYNTNMGAKFRQLMFEHISCLTFGRETVIEYL 120
Oy 61 CWMGLMTLATVWGVNLDPASRDLVSVYNTNMGAKFRQLMFEHISCLTFGRETVIEYL 120
||:|||||
121 SFGWIRTPPPAYRPNNAPILSTLPETTVYRRKGTTPRRRTDPSPPRRRSQSPRRRSQSR 180
Oy 121 SFGWIRTPPPAYRPNNAPILSTLPETTVYRRKGRSPRRRTDPSPPRRRSQSPRRRSQSR 180
||:|||||
Db 181 SOC 183
Oy 181 SOC 183

RESULT 7
ENTRY       S53216 #type complete
TITLE       e antigen precursor / core antigen - hepatitis B virus
            (isolate patient Castag'3)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen; pre-C/C antigen
CONTAINS       core antigen; e antigen
ORGANISM       #formal_name hepatitis B virus; HBV
VARIETY        isolate patient Castag'3
DATE          08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
            08-Sep-1997

ACCESSIONS   S53216
REFERENCE    S53112
#authors     Lai, M.E.; Mazzioleni, A.P.; Porru, A.; Balestrieri, A.
#submission  Submitted to the EMBL Data Library, March 1995
#accession   S53216
#molecule_type DNA
#residues   1-212
#cross-references EMBL:X85293; NID:q736124; PID:q736126
#experimental_source isolate patient Castag'3

GENETICS
CLASSIFICATION C
KEYWORDS       #superfamily hepatitis B virus core antigen
               alternative initiators; core protein
FEATURE        #domain signal sequence #status predicted #label STG\
               #product core antigen #status predicted #label CAG\
               #product e antigen #status predicted #label ENG\
               #domain carboxyl-terminal propeptide #link EXG #status
               predicted #label ECP
SUMMARY        #length 212 #molecular-weight 24363 #checksum 752

Query Match      46.0%; Score 1370; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.39e-205;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db	29	GMDIDPYKEFGATYELLSEFLPSDFPSYRDLDDNASALYREALESPHCSPHHTALROAI	88
Oy	213	SMIDIDPYKEFGATYELLSEFLPSDFPSYRDLDDNASALYREALESPHCSPHHTALROAI	272
Db	89	LCWGLMLTLAWGAVNEDPASRLVVSYYVTNNGLGFROLMLFHSICLTFGRETVEYL	148
Oy	273	LCWGLMLTLAWGAVNEDPASRLVVSYYVTNNGLGFROLMLFHSICLTFGRETVEYL	332
Db	149	VSFQWIRTPAYRPNAPNPIILSTLPETTVYRRRGRSRRRTPPSPRRRSQSPRRRSQSR	208
Oy	333	VSFQWIRTPAYRPNAPNPIILSTLPETTVYRRRGRSRRRTPPSPRRRSQSPRRRSQSR	392
Db	209	ESQC 212	
Oy	393	ESQC 396	
RESULT	8		
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ALTERNATE_NAMES			
CONTAINS			
ORGANISM			
DATE			
ACCESSIONS			
REFERENCE			
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GENETICS			
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CLASSIFICATION			
KEYWORDS			
FEATURE			
1-29			
30-212			
30-218			
179-212			
SUMMARY			
Query Match			
Best local similarity			
Matches			
Db	29	GMDIDPYKEFGATYELLSEFLPSDFPSYRDLDDNASALYREALESPHCSPHHTALROAI	88
Oy	213	SMIDIDPYKEFGATYELLSEFLPSDFPSYRDLDDNASALYREALESPHCSPHHTALROAI	272
Db	89	LCWGLMLTLAWGAVNEDPASRLVVSYYVTNNGLGFROLMLFHSICLTFGRETVEYL	148
Oy	273	LCWGLMLTLAWGAVNEDPASRLVVSYYVTNNGLGFROLMLFHSICLTFGRETVEYL	332
Db	149	VSFQWIRTPAYRPNAPNPIILSTLPETTVYRRRGRSRRRTPPSPRRRSQSPRRRSQSR	208
Oy	333	VSFQWIRTPAYRPNAPNPIILSTLPETTVYRRRGRSRRRTPPSPRRRSQSPRRRSQSR	392
Db	209	ESQC 212	
Oy	393	ESQC 396	
RESULT	9		
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TITLE			
ALTERNATE_NAMES			
CONTAINS			
ORGANISM			
DATE			
ACCESSIONS			
REFERENCE			
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#accession			
#molecules			
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CLASSIFICATION			
KEYWORDS			
FEATURE			
1-29			
30-212			
30-218			
179-212			
SUMMARY			
Query Match			
Best local similarity			
Matches			
Db	29	GMDIDPYKEFGATYELLSEFLPSDFPSYRDLDDNASALYREALESPHCSPHHTALROAI	88
Oy	213	SMIDIDPYKEFGATYELLSEFLPSDFPSYRDLDDNASALYREALESPHCSPHHTALROAI	272
Db	89	LCWGLMLTLAWGAVNEDPASRLVVSYYVTNNGLGFROLMLFHSICLTFGRETVEYL	148
Oy	273	LCWGLMLTLAWGAVNEDPASRLVVSYYVTNNGLGFROLMLFHSICLTFGRETVEYL	332
Db	149	VSFQWIRTPAYRPNAPNPIILSTLPETTVYRRRGRSRRRTPPSPRRRSQSPRRRSQSR	208
Oy	333	VSFQWIRTPAYRPNAPNPIILSTLPETTVYRRRGRSRRRTPPSPRRRSQSPRRRSQSR	392
Db	209	ESQC 212	
Oy	393	ESQC 396	
RESULT	9		
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TITLE			
ALTERNATE_NAMES			
CONTAINS			
ORGANISM			
DATE			
ACCESSIONS			
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#submitted			
#accession			
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#cross-references			
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CLASSIFICATION			
KEYWORDS			
FEATURE			
1-29			
30-212			
30-218			
179-212			
SUMMARY			
Query Match			
Best local similarity			
Matches			
Db	29	GMDIDPYKEFGATYELLSEFLPSDFPSYRDLDDNASAL	

Db	149	VSGFWITPPAYRPNNPIIISTLPETTVARRGRGSPRRRTPSPRRRSQSPRRRSQSR	208
Oy	333	VSGFWITPPAYRPNNPIIISTLPETTVARRGRGSPRRRTPSPRRRSQSPRRRSQSR	392
Db	209	ESQC 212	
Oy	393	ESQC 396	
RESULT	12		
ENTRY		S53198	#type complete
TITLE		e antigen precursor / core antigen - hepatitis B virus (isolate patient Ferracuti-2'90)	
ALTERNATE_NAMES		HBE antigen precursor / HBC antigen; pre-C/C antigen	
CONTAINS		core antigen; e antigen	
ORGANISM		#formal_name hepatitis B virus, HBV	
DATE		isolate patient Ferracuti-2'90	
		08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change	
		08-Sep-1997	
ACCESSIONS		S53198	
REFERENCE		S53112	
#authors		Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.	
#submitter		submitted to the EMBL Data Library, March 1995	
#accession		S53198	
#molecule_type		DNA	
#residues		1-212 #label LAI	
#cross-references		EMBL:X85285; NID:g736099; PID:g736100	
#experimental_source		isolate patient Ferracuti-2'90	
GENETICS			
#gene		C	
CLASSIFICATION		#superfamily hepatitis B virus core antigen	
KEYWORDS		alternative initiators; core protein	
FEATURE			
1-29		#domain signal sequence #status predicted #label SIG\	
30-212		#product core antigen #status predicted #label CAG\	
30-178		#product e antigen #status predicted #label ENG\	
179-212		#domain carboxyl-terminal propeptide #link ENG #status	
		predicted #label ECP	
SUMMARY		#length 212 #molecular_weight 24292 #checksum 593	
Query Match		46.0%; Score 1368; DB 2; Length 212;	
Best Local Similarity		98.4%; Pred. No. 3,086-205;	
Matches		181; Conservative 2; Mismatches 1; Indels 0; Gaps 0	
Db	29	GMDIDPYKFGATVLLSFDSAFPPSYRDLDITASALYREALSEPHHCSPHHTLRQAI	88
Oy	213	SMDDIPYKEFGATVLLSFSDPFSYRDLDITASALYREALSEPHHCSPHHTLRQAI	272
Db	89	LCMGDLMTLATVGNLEDPASRDLVSVYVMNMGKRLQMLPFHISCTLTGRETVEYL	148
Oy	273	LCMGELMTLATVGNLEDPASRDLVSVYVMNMGKRLQMLPFHISCTLTGRETVEYL	332
Db	149	VSGFWITPPAYRPNNPIIISTLPETTVARRGRGSPRRRTPSPRRRSQSPRRRSQSR	208
Oy	333	VSGFWITPPAYRPNNPIIISTLPETTVARRGRGSPRRRTPSPRRRSQSPRRRSQSR	392
Db	209	ESQC 212	
Oy	393	ESQC 396	
RESULT	13		
ENTRY		S53223	#type complete
TITLE		e antigen precursor / core antigen - hepatitis B virus (isolate patient Chigline-1'85)	
ALTERNATE_NAMES		HBE antigen precursor / HBC antigen; pre-C/C antigen	
CONTAINS		core antigen; e antigen	
ORGANISM		#formal_name hepatitis B virus, HBV	
DATE		isolate patient Chigline-1'85	
		08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change	
		08-Sep-1997	
ACCESSIONS		S53223	

REFERENCE	553112	Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#authors	Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.	
#submission	submitted to the EMBL Data Library, March 1995	
#accession	S53223	
#molecule_type	DNA	
#residues	1-212	#label LAI
#cross-references	EMBL:X85295; NID:g736134; PID:g736136	
#experimental_source	isolate patient Chigline-1'85	
GENETICS		
CLASSIFICATION	C	#superfamily hepatitis B virus core antigen
KEYWORDS	alternative initiators; core protein	
FEATURE		
1-29		#domain signal sequence #status predicted #label SIG\
30-212		#product core antigen #status predicted #label CAG\
30-178		#product e antigen #status predicted #label EAG\
179-212		#domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP
SUMMARY	#length 212	#molecular-weight 24364 #checksum 1123
Query Match	45.9%	Score 1366; DB 2; Length 212;
Best Local Similarity	97.8%	Pred. No. 6,81e-205;
Matches 180;	Conservative 3;	Mismatches 1; Indels 0; Gaps 0
Db	29 GMDIDPYKFGATVELLSFLPSDFEPPSVRDDLDTRASALYREALSPHCSPHTRALQAI	88
Oy	213 SMDIDPYKFGATVELLSFLPSDFEPPSVRDDLDTRASALYREALSPHCSPHTRALQAI	272
Db	89 LCMGDLMLATWGVNLDPSRDLVSVYVNTNMGKLRQLMFIISCLTGTGREVIEYL	148
Oy	273 LCMGDLMLATWGVNLDPSRDLVSVYVNTNMGKLRQLMFIISCLTGTGREVIEYL	332
Db	149 VSFQWIRTPPYRPNPILSTLPTETVYVRRGSPRRTPSPRRRSQSPRRRSQSR	208
Oy	333 VSFQWIRTPPYRPNPILSTLPTETVYVRRGSPRRTPSPRRRSQSPRRRSQSR	392
Db	209 ESQC 212	
Oy	393 ESQC 396	
RESULT 14		
ENTRY	S53274	#type complete
TITLE	e antigen precursor / core antigen - hepatitis B virus (isolate patient Giordo'84)	
ALTERNATE_NAMES	HBe antigen precursor / HBe antigen; pre-C/C antigen	
CONTAINS	core antigen; e antigen	
ORGANISM	#formal_name hepatitis B virus, HBV	
DATE	isolate patient Giordo'84	
	08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997	
ACCESSIONS	S53274	
REFERENCE	S53112	
#authors	Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.	
#submission	submitted to the EMBL Data Library, March 1995	
#accession	S53274	
#molecule_type	DNA	
#residues	1-212	#label LAI
#cross-references	EMBL:X85316; NID:g736208; PID:g736210	
#experimental_source	isolate patient patient Giordo'84	
GENETICS		
CLASSIFICATION	C	#superfamily hepatitis B virus core antigen
KEYWORDS	alternative initiators; core protein	
FEATURE		
1-29		#domain signal sequence #status predicted #label SIG\
30-212		#product core antigen #status predicted #label CAG\
30-178		#product e antigen #status predicted #label EAG\
179-212		#domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP
SUMMARY	#length 212	#molecular-weight 24376 #checksum 390
Query Match	45.9%	Score 1366; DB 2; Length 212;

Best Local Similarity 98.9% Pred. No. 6 81e-205;
Matches 182: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHCSPHHTALROAI 88
OY 213 SMDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHCSPHHTALROAI 272
Db 89 LCWGEIATMTATWGVNLEDPSARDLVSYVNTMGLKFRQLMFHISCLTFGRETIVIEYL 148
OY 273 LCWGEIATMTATWGVNLEDPSARDLVSYVNTMGLKFRQLMFHISCLTFGRETIVIEYL 332
Db 149 VSFGVWIRTPPAYRPPNAPILITLPTETVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 208
OY 333 VSFGVWIRTPPAYRPPNAPILITLPTETVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 392
Db 209 ESOC 212
OY 393 ESOC 396

RESULT 15
ENTRY S53169 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Muresu '89)
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Muresu '89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53169
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53169
##molecule_type DNA
##residues 1-183 ##label LAI
##cross_references EMBL:X85275; NID:g736057; PID:g736060
##experimental_source isolate patient Muresu '89
#note due to a stop codon between the alternative initiators the e antigen precursor cannot be produced

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
SUMMARY #length 183 #molecular_weight 21088 #checksum 1849

Query Match 45.8% Score 1364; DB 2; Length 183;
Best Local Similarity 98.4% Pred. No. 1.51e-204;
Matches 180: Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHCSPHHTALROAI 60
OY 1 MDIDPYKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHCSPHHTALROAI 60
Db 61 CWGEIATMTATWGVNLEDPSARDLVSYVNTMGLKFRQLMFHISCLTFGRETIVIEYL 120
OY 61 CWGEIATMTATWGVNLEDPSARDLVSYVNTMGLKFRQLMFHISCLTFGRETIVIEYL 120
Db 121 SFGVWIRTPPAYRPPNAPILITLPTETVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 180
OY 121 SFGVWIRTPPAYRPPNAPILITLPTETVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 180
Db 181 SQC 183
OY 181 SQC 183

Search completed: Thu Dec 16 12:48:36 1999
Job time : 77 secs.

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Cap 11

Listing first 45

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Test Local Sim11

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTAL 60
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QY 1 MDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTAL 60
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QY 61 CMGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETVIEYLV 120
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRSOSRE 180
  121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRSOSRE 180
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRSOSRE 180
Db 181 SOC 183
  181 SOC 183
QY 181 SOC 183
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RESULT 2
ID CORA_HPBVA STANDARD; PRT; 211 AA.
AC P24023;
DT 01-MAR-1992 (REL. 21, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (STRAIN ALPHA).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90266476.
RA TONG S., LI J., VIRIVINSKI L., TREPO C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is associated with viral variants containing an inactive pre-C region";
RL VIROLOGY 176:596-603(1990).

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CC
CC EMBL; M32138; G495034; ALT_SEQ.
CC PIR; A34773; NKVLAI.
DR PFAM; PF00906; Hepatitis_core; 1.
DR CORE PROTEIN; REPEAT
FT REPEAT 183 190
FT REPEAT 198 206
SQ SEQUENCE 211 AA; 24208 MW; 0924CE5E CRC32;

Query Match 45.6%; Score 1358; DB 1; Length 211;
Best Local Similarity 95.2%; Pred. No. 2.35e-233;
Matches 179; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db 24 LGWLDMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTAL 83
  1 LGWLDMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTAL 83
QY 209 LGWLDMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTAL 268
Db 84 RQAILCGMDLITLSTWGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETV 143
  84 RQAILCGMDLITLSTWGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETV 143
QY 269 RQAILCGMDLITLSTWGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETV 328
Db 144 IEVLVSGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRR 203
  144 IEVLVSGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRR 203
QY 329 IEVLVSGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRR 388
Db 204 TOSRESOC 211
  204 TOSRESOC 211
QY 389 SOSRESOC 396
  389 SOSRESOC 396

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RESULT 3
ID CORA_HPBVA STANDARD; PRT; 183 AA.
AC P03147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81012115.
RA PASEK M., GOTO T., GILBERT W., ZINK B., SCHALLER H., MCKAY P.,
RA LEADBETTER G., MURRAY K.;
RT "Hepatitis B virus genes and their expression in E. coli";
RL NATURE 282:575-579(1979).

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CC
CC EMBL; J02202; G329638; -
CC EMBL; A08967; G411874; -
DR PIR; B93217; NKVLA2
DR PFAM; PF00906; Hepatitis_core; 1.
DR CORE PROTEIN; REPEAT
KW REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21042 MW; 6EA6B674 CRC32;

Query Match 45.3%; Score 1349; DB 1; Length 183;
Best Local Similarity 96.7%; Pred. No. 1.41e-231;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTAL 60
  1 MDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTAL 60
QY 1 MDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTAL 60
Db 61 CMGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETVIEYLV 120
  61 CMGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETVIEYLV 120
QY 61 CMGELMTLATWGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETVIEYLV 120
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRSOSRE 180
  121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRSOSRE 180
QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSOSPRRRSOSRE 180
Db 181 SOC 183
  181 SOC 183
QY 181 SOC 183
  181 SOC 183

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RESULT 4
ID CORA_HPBVA STANDARD; PRT; 183 AA.
AC P17392;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN OKINAWA/P0DW282).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., YAIYU M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes";

RL J. GEN. VIROL. 69:2575-2583(1988).
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 CC -----
 CC EMBL: D00330; NOT_ANNOTATED_CDS.
 DR PIR: B28925; NKVLJ2.
 DR PFAM: PF00906; Hepatitis_core; 1.
 KW CORE PROTEIN; REPEAT.
 FT REPEAT 162 169
 FT REPEAT 170 177
 SQ SEQUENCE 183 AA; 21081 MW; 115BD9E3 CRC32;
 Query Match 44.98; Score 1336; DB 1; Length 183;
 Best Local Similarity 96.28; Pred. No. 5,22e-229;
 Matches 176; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MDIDPKKEFGASYELLSELPDFFPSYRDLLDTASALYREALSPCHSHHTALRAIL 60
 QY 1 MDIDPKKEFGATVELLSFLPSDFPSYRDLLDTASALYREALSPCHSHHTALRAIL 60
 Db 61 CWGELMNLATWGSNLEDPASRELIVSYVNVNMGKIRQLMFIHSCLTGREVIEYL 120
 QY 61 CWGELMNLATWGVNLEDPASRDLYSVYVNTNMGKIRQLMFIHSCLTGREVIEYL 120
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRTPSPRRRSQSRRRSQSRE 180
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRTPSPRRRSQSRRRSQSRE 180
 Db 181 SOC 183
 QY 181 SOC 183
 RESULT 5
 ID CORA_HPBV4 STANDARD; PRT; 183 AA.
 AC P03150; P03151;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN C.
 OS HEPATITIS B VIRUS (SUBTYPE ADP), HEPATITIS B VIRUS (SUBTYPE ADP4),
 OS AND HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN INDONESIA/P1DW420).
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ADR:
 RC MEDLINE: 83168919
 RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 RT DNA: subtype adr and adw.";
 RL NUCLEIC ACIDS RES. 11:1747-1757(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ADR4;
 RC MEDLINE: 83246570.
 RA FUJUYAMA A., MIYANOHARA A., NOZAKI C., YONEYAMA T., OHTOMO N.,
 RA MATSUBARA K.;
 RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
 RT adr.";
 RL NUCLEIC ACIDS RES. 11:4601-4610(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ADM;
 RC MEDLINE: 89010694.
 RA OKAMOTO H., TSUDA F., SAKUGAMA H., SASUROSEWIGNTO R.I., IMAI M.,
 RA MIYAKAWA Y., NAYUMI M.;

RT "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. GEN. VIROL. 69:2575-2583(1988).
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 CC -----
 CC EMBL: V00867; NOT_ANNOTATED_CDS.
 DR EMBL: X01587; G59407; .
 DR EMBL: D00331; NOT_ANNOTATED_CDS.
 DR PIR: A93480; NKVLAS.
 DR PIR: B93460; NKVL44.
 DR PIR: C28925; NKVLJ3.
 DR PFAM: PF00906; Hepatitis_core; 1.
 KW CORE PROTEIN; REPEAT.
 FT REPEAT 162 169
 FT REPEAT 170 177
 SQ SEQUENCE 183 AA; 21095 MW; D2E185B9 CRC32;
 Query Match 44.88; Score 1334; DB 1; Length 183;
 Best Local Similarity 95.68; Pred. No. 1.30e-228;
 Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MDIDPKKEFGASYELLSELPDFFPSYRDLLDTASALYREALSPCHSHHTALRAIL 60
 QY 1 MDIDPKKEFGATVELLSFLPSDFPSYRDLLDTASALYREALSPCHSHHTALRAIL 60
 Db 61 CWGELMNLATWGSNLEDPASRELIVSYVNVNMGKIRQLMFIHSCLTGREVIEYL 120
 QY 61 CWGELMNLATWGVNLEDPASRDLYSVYVNTNMGKIRQLMFIHSCLTGREVIEYL 120
 Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRTPSPRRRSQSRRRSQSRE 180
 QY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRTPSPRRRSQSRRRSQSRE 180
 Db 181 SOC 183
 QY 181 SOC 183
 RESULT 6
 ID CORA_HPBVJ STANDARD; PRT; 183 AA.
 AC P17351;
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN C.
 OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN JAPAN/PJDM233).
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 89010694.
 RA OKAMOTO H., TSUDA F., SAKUGAMA H., SASUROSEWIGNTO R.I., IMAI M.,
 RA MIYAKAWA Y., NAYUMI M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. GEN. VIROL. 69:2575-2583(1988).
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 CC -----
 CC EMBL: D00329; NOT_ANNOTATED_CDS.
 DR PIR: A28925; NKVLJ1.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN; REPEAT
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA: 21224 MW: F6B348B6 CRC32;

Query Match 44.4%; Score 1322; DB 1; Length 183;

Best Local Similarity 96.2%; Pred. No. 3.03e-226;
Matches 176; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 MDIDPKKGAIVELLSPDSDFPSVRLDLDTSALYREALSPHCSPHNTALROAIL 60
OY 1 MDIDPKKGAIVELLSPDSDFPSVRLDLDTSALYREALSPHCSPHNTALROAIL 60
Db 61 CGEGLMTLATWGNLLEDPASRDLYVNYVTNKGKIRQLMWHISCLTFGRRTVLEYIV 120
OY 61 CGEGLMTLATWGNLLEDPASRDLYVNYVTNKGKIRQLMWHISCLTFGRRTVLEYIV 120
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOSRE 180
OY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOSRE 180
Db 181 SOC 183
OY 181 SOC 183

RESULT 7
ID CORA_HPBVM STANDARD; PRT; 185 AA.

AC P03149;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.

OS HEPATITIS B VIRUS (SUBTYPE ADW).

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83168919.

RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;

RT "The complete nucleotide sequences of the cloned hepatitis B virus
DNA: subtype adr and adv";

RL NUCLEIC ACIDS RES. 11:1747-1757(1983).

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CC EMBL: V00866; NOT_ANNOTATED_CDS.

DR PIR: C93460; NKVLA6.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN; REPEAT

FT REPEAT 164 171

FT REPEAT 172 179

SQ SEQUENCE 185 AA: 21394 MW: 791E0381 CRC32;

Query Match 44.4%; Score 1321; DB 1; Length 185;

Best Local Similarity 96.2%; Pred. No. 4.78e-226;
Matches 178; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Db 1 MDIDPKKGAIVELLSPDSDFPSVRLDLDTSALYREALSPHCSPHNTALROAIL 60
OY 1 MDIDPKKGAIVELLSPDSDFPSVRLDLDTSALYREALSPHCSPHNTALROAIL 60
Db 61 CGEGLMTLATWGNLLEDPASRDLYVNYVTNKGKIRQLMWHISCLTFGRRTVLEYIV 120
OY 61 CGEGLMTLATWGNLLEDPASRDLYVNYVTNKGKIRQLMWHISCLTFGRRTVLEYIV 120
Db 61 CGEGLMTLATWGNLLEDPASRDLYVNYVTNKGKIRQLMWHISCLTFGRRTVLEYIV 120
OY 61 CGEGLMTLATWGNLLEDPASRDLYVNYVTNKGKIRQLMWHISCLTFGRRTVLEYIV 120

Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOS 180
OY 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOS 178
Db 181 RESOC 185
OY 179 RESOC 183

RESULT 8
ID CORA_HPBVM STANDARD; PRT; 195 AA.

AC P29178;

DT 01-DEC-1992 (REL. 24, CREATED)

DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)

DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

GN C.

OS HEPATITIS B VIRUS (SUBTYPE ADW2 VARIANT SF).

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE: 90169850.

RA BHAT R.A., ULRICH P.P., VYAS G.N.;

RT "Molecular characterization of a new variant of hepatitis B virus in
a persistently infected homosexual man.";

RL HEPATOLOGY 11:271-276(1990).

DR PIR: A37182; NKVLA3.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN; REPEAT

FT REPEAT 174 181

FT REPEAT 182 189

SQ SEQUENCE 195 AA: 22461 MW: AF3DB5F3 CRC32;

Query Match 44.1%; Score 1314; DB 1; Length 195;

Best Local Similarity 93.5%; Pred. No. 1.15e-224;
Matches 173; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 11 FGLDIDPKKGAIVELLSPDSDFPSVRLDLDTSALYREALSPHCSPHNTALROAIL 70
OY 212 LMSDIDPKKGAIVELLSPDSDFPSVRLDLDTSALYREALSPHCSPHNTALROAIL 271

Db 71 ILCWEGLMTLATWGNLLEDPASRDLYVNYVTNKGKIRQLMWHISCLTFGRRTVLEY 130
OY 272 ILCWEGLMTLATWGNLLEDPASRDLYVNYVTNKGKIRQLMWHISCLTFGRRTVLEY 331

Db 131 IVSFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOS 190
OY 332 IVSFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOS 391

Db 191 RESOC 195

OY 392 RESOC 396

RESULT 9
ID CORA_HPBVM STANDARD; PRT; 212 AA.

AC Q03495;

DT 01-NOV-1995 (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

GN C.

OS HEPATITIS B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE W4B).

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE: 93346970.

RA NAUMANN H., SCHAEFER S., YOSHIDA C.F.T., GASPAR A.M.C., REPP R.,

RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
that expresses HBV surface antigen subtype adw4.";

RL J. GEN. VIROL. 74:1627-1632(1993).

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DR EMBL: X69798; G59423; -
DR PFAM: PF00906; Hepatitis_core: 1.
KW CORE PROTEIN: REPEAT.
FT DOMAIN 178 204 ARG-RICH.
FT REPEAT 184 203 3 X 5 AA REPEATS OF S-P-R-R-R.
FT REPEAT 184 188 1.
FT REPEAT 191 195 2.
FT REPEAT 199 203 3.
SQ SEQUENCE 212 AA; 24234 MW; BCCDF263 CRC32;

Query Match 44.1%; Score 1313; DB 1; Length 212;
Best Local Similarity 92.9%; Pred. No. 1,81e-224;
Matches 171; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
QY 213 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 272
Db 89 LCMGELMTASVGNLLEDPASRDLVSVYNTNMGKIRQLMFHISCLTFGRVIEYLV 148
QY 273 LCMGELMTATVGNLLEDPASRDLVSVYNTNMGKIRQLMFHISCLTFGRVIEYLV 332
Db 149 VSGWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSP 208
QY 333 VSGWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSP 392
Db 209 ASOC 212
QY 393 ESOC 396

RESULT 10
ID CORA_HPBVL STANDARD; PRT: 183 AA.
AC P12901;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (STRAIN LSH / CHIMPANZEE ISOLATE).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88258473.
RA VAUDIN M., WOLSTEINHOE A.J., TSIOUVE K.N., ZUCKERMAN A.J.,
RA HARRISON T.J.;
RT "The complete nucleotide sequence of the genome of a hepatitis B
RT virus isolated from a naturally infected chimpanzee";
RL J. GEN. VIROL. 69:1383-1389(1988).
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DR EMBL: D00220; D1000603; -
DR PIR: A28885; NKVLCF.
DR PFAM: PF00906; Hepatitis_core: 1.
KW CORE PROTEIN: REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 20999 MW; 1AF57C9 CRC32;

Query Match 43.9%; Score 1308; DB 1; Length 183;
Best Local Similarity 94.5%; Pred. No. 1.76e-223;
Matches 173; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
Db 61 CMGELMTATVGNLLEDPASRDLVSVYNTNMGKIRQLMFHISCLTFGRVIEYLV 120
QY 61 CMGELMTATVGNLLEDPASRDLVSVYNTNMGKIRQLMFHISCLTFGRVIEYLV 120
Db 121 SFGWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSPA 180
QY 121 SFGWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSPA 180
Db 181 SOC 183
QY 181 SOC 183

RESULT 11
ID CORA_HPBV2 STANDARD; PRT: 185 AA.
AC P03148;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADM2).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA VALENZUELA P., QUIROGA M., ZALDIVAR J., GRAY P., RUTTER W.J.;
RL (IN) FIELD B.N., JAKENICH R., FOX C.F. (EDS.);
RL ANIMAL VIRUS GENETICS, PP. 57-70, ACADEMIC PRESS, NEW YORK (1980).
DR PIR: A94409; NKVLA3.
DR PFAM: PF00906; Hepatitis_core: 1.
KW CORE PROTEIN: REPEAT.
FT REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; E2EA3360 CRC32;

Query Match 43.8%; Score 1305; DB 1; Length 185;
Best Local Similarity 95.7%; Pred. No. 6.88e-223;
Matches 177; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Db 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
QY 1 MDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
Db 61 CMGELMTATVGNLLEDPASRDLVSVYNTNMGKIRQLMFHISCLTFGRVIEYLV 120
QY 61 CMGELMTATVGNLLEDPASRDLVSVYNTNMGKIRQLMFHISCLTFGRVIEYLV 120
Db 121 SFGWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSPA 180
QY 121 SFGWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSPA 178
Db 181 RESOC 185
QY 179 RESOC 183

RESULT 12
ID CORA_HPBV9 STANDARD; PRT: 214 AA.
AC P17099;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.

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OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN 991).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RA SEQUENCE FROM N.A.
RX KOEHEL H.G., SCHUELER A., LOTTMANN S., THOMSEN R.;
RL SUBMITTED (FEB-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
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CC -----
DR EMBL: X51970; G60433; -
DR PIR: S10381; NKVLK5; -
DR PFAM: PF00906; Hepatitis_core; 1.
DR CORE PROTEIN; REPEAT.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 786CD048 CRC32;

Query Match 43.8%; Score 1304; DB 1; Length 214;
Best Local Similarity 95.2%; Pred. No. 1,08e-222;
Matches 177; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Db 29 GMDIPKKEGATVELLSPDSEFFSVRLDLPDASALYREALSPHCSPHHTALROAI 88
QY 213 SMDIPKKEGATVELLSPDSEFFSVRLDLPDASALYREALSPHCSPHHTALROAI 272
Db 89 LCMGELMTLATWGNLDEPDASRDLVVNYVNTNGLKIRQLMFRISYLTFFGRTVLEYL 148
QY 273 LCMGELMTLATWGNLDEPDASRDLVVNYVNTNGLKIRQLMFRISYLTFFGRTVLEYL 332
Db 149 VSGEWMRTPPAPRPAPNPILSTLPETTVARRRGRSPRRRTSPRRRSQSPRRRSQ 208
QY 333 VSGEWMRTPPAPRPAPNPILSTLPETTVARRR--GRSPRRRTSPRRRSQSPRRRSQ 390
Db 209 SRESOC 214
QY 391 SRESOC 396

RESULT 13
ID CORA_MHV1 STANDARD; PRT; 188 AA.
AC P03152;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 1 (MHV 1),
OS WOODCHUCK HEPATITIS VIRUS 7 (MHV 7),
OS WOODCHUCK HEPATITIS VIRUS 59 (MHV 59), AND
OS WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE) (MHV 8).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RA SEQUENCE FROM N.A.
RX SPECIES=WOODCHUCK HEPATITIS VIRUS 1;
RL MEDLINE: 82216969.
RA GALIBERT F., CHEN T.N., MANDART E.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT comparison with the hepatitis B virus sequence.";
RL J. VIROL. 41:51-65(1982).

RN 12]
RP SEQUENCE FROM N.A.
RX SPECIES=WOODCHUCK HEPATITIS VIRUS 7, AND WOODCHUCK HEPATITIS VIRUS 59;
RX MEDLINE: 88101359.
RX COHEN J.J., MILLER R.H., ROSENBLUM B., DENNISTON K., GERIN J.L.,
RA PURCELL R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RT shows conservation of the genome.";

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RL VIROLOGY 162:12-20(1988).
RN [3]
RA SEQUENCE FROM N.A.
RX SPECIES=WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE);
RX MEDLINE: 89184524.
RA GIROUX R., COTE P.J., HORNBUCKLE W.E., TENNANT B.C., GERIN J.L.,
RA PURCELL R.H., MILLER R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RT hepatitis virus that is infectious in the natural host.";
RL PROC. NTL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
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CC -----
DR EMBL: J02442; G336129; -
DR EMBL: M18752; G336140; -
DR EMBL: M19183; G336145; -
DR EMBL: J04514; G336149; -
DR PIR: A03713; NKVLC.
DR PIR: C32397; NKVLC4.
DR PIR: C32397; NKVLC3.
DR PFAM: PF00906; Hepatitis_core; 1.
DR CORE PROTEIN; REPEAT.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; A667DB27 CRC32;

Query Match 31.5%; Score 938; DB 1; Length 188;
Best Local Similarity 67.0%; Pred. No. 6,28e-151;
Matches 126; Conservative 25; Mismatches 32; Indels 5; Gaps 1;

Db 1 MDIPKKEGSSYQLNPLDPEFDLNLVDITALYEBELTGRCSPHHTALROAI 60
QY 1 MDIPKKEGATVELLSPDSEFFSVRLDLPDASALYREALSPHCSPHHTALROAI 60
Db 61 CMDELTKLIAMSSNTSEVRIIVNHVDIWLGLVROSLMHSCLTFGGTVOEFLY 120
QY 61 CMGELMTLATWGNLDEPDASRDLVVNYVNTNGLKIRQLMFRISYLTFFGRTVLEYL 120
Db 121 SFGVMRTPPAPRPAPNPILSTLPETTVARRRGRSARRRTPSPRRRSQSPRRRR 180
QY 121 SFGVMRTPPAPRPAPNPILSTLPETTVARRG-----RSPRRRTSPRRRSQSPRRRR 175
Db 181 SOSPSANC 188
QY 176 SOSRESOC 183

RESULT 14
ID CORA_HPV8 STANDARD; PRT; 217 AA.
AC P03153;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS GROUND SQUIRREL HEPATITIS VIRUS (GSHV).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RA SEQUENCE FROM N.A.
RX MEDLINE: 84267998.
RX SEEGER C., GANEM D., YAMUS H.E.;
RT "Nucleotide sequence of an infectious molecularly cloned genome of
RT ground squirrel hepatitis virus.";
RL J. VIROL. 51:367-375(1984).
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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Dec 16 12:50:17 1999; Maspar time 26.61 Seconds
 Tabular output not generated. 812.364 Million cell updates/sec

Title: >US38183-1-38183
 Description: (1-396) from us38183-1-38183.pep
 Perfect Score: 2977
 Sequence: 1 MDIDPKKFGATVELLSFLP.....RRRSQSPRRRRSQSRESQC 396

Scoring table: PAM 150
 Gap 11

Searched: 179066 seqs, 54579741 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: splrembl9
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 46.585; Variance 101.482; scale 0.459
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1375	46.2	212 14	089656	PRE-C/CORE.	2.16e-231
2	1374	46.2	212 14	088020	PRE-C/CORE.	3.37e-231
3	1374	46.2	212 14	089537	HBCAG.	3.37e-231
4	1373	46.1	183 14	089437	X, PREC AND C GENES (C	5.26e-231
5	1373	46.1	183 14	068008	X, PREC AND C GENES (F	5.26e-231
6	1373	46.1	212 14	067872	PRE C/C ORF.	5.26e-231
7	1372	46.1	212 14	011884	CORE ANTIGEN PRECURSOR	8.20e-231
8	1370	46.0	183 14	068056	X, PREC AND C GENES (L	1.99e-230
9	1370	46.0	212 14	068058	PRE-C/CORE.	1.99e-230
10	1370	46.0	212 14	068025	PRE-C/CORE.	1.99e-230
11	1369	46.0	212 14	067872	PRE C/C ORF.	3.11e-230
12	1369	46.0	212 14	067984	PRE-C/CORE.	3.11e-230
13	1369	46.0	212 14	068032	PRE-C/CORE.	3.11e-230
14	1368	46.0	212 14	068010	PRE-C/CORE.	4.85e-230
15	1366	45.9	212 14	068070	PRE-C/CORE.	1.18e-229
16	1366	45.9	212 14	068030	PRE-C/CORE.	1.18e-229
17	1364	45.8	183 14	067989	X, PREC AND C GENES (M	2.86e-229
18	1363	45.8	183 14	068048	X, PREC AND C GENES (F	4.46e-229
19	1363	45.8	212 14	068014	PRE-C/CORE.	4.46e-229
20	1363	45.8	212 14	068012	PRE-C/CORE.	4.46e-229

21	1363	45.8	212 14	067980	PRE-C/CORE.	4.46e-229
22	1362	45.8	212 14	068051	PRE-C/CORE.	6.96e-229
23	1360	45.7	212 14	089446	PRE-C/CORE.	1.69e-228
24	1360	45.7	212 14	068016	PRE-C/CORE.	1.69e-228
25	1360	45.7	212 14	096845	COMPLETE GENOME.	1.69e-228
26	1359	45.6	212 14	068053	PRE-C/CORE.	2.64e-228
27	1357	45.6	212 14	068075	PRE-C/CORE.	6.41e-228
28	1357	45.6	212 14	068077	PRE-C/CORE.	6.41e-228
29	1355	45.5	212 14	068045	PRE-C/CORE.	1.56e-227
30	1352	45.4	183 14	089531	CORE PROTEIN.	5.90e-227
31	1351	45.4	183 14	067946	C ANTIGEN.	9.20e-227
32	1351	45.4	212 14	089719	PRE-C/CORE.	9.20e-227
33	1349	45.3	183 14	067997	X, PREC AND C GENES (B	2.24e-226
34	1348	45.3	183 14	068037	X, PREC AND C GENES (D	3.49e-226
35	1348	45.3	183 14	068030	X, PREC AND C GENES (M	3.49e-226
36	1345	45.2	183 14	067973	X, PREC AND C GENES (T	1.32e-225
37	1347	45.2	212 14	067912	PRE-CORE/CORE PROTEIN.	5.43e-226
38	1343	45.1	183 14	068023	X, PREC AND C GENES (C	3.21e-225
39	1342	45.1	183 14	067964	X, PREC AND C GENES (F	5.06e-225
40	1344	45.1	212 14	092918	PRECORE PROTEIN PRECUR	2.06e-225
41	1344	45.1	212 14	068035	PRE-C/CORE.	2.06e-225
42	1341	45.0	183 14	068064	X, PREC AND C GENES (S	7.80e-225
43	1341	45.0	183 14	068003	X, PREC AND C GENES (L	7.80e-225
44	1341	45.0	212 14	068042	PRE-C/CORE.	7.80e-225
45	1341	45.0	212 14	081115	HBCAG,HBCAG.	7.80e-225

ALIGNMENTS

RESULT 1
 ID 089656; PRELIMINARY; PRT; 212 AA.
 AC 089656;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PRE-C/CORE.
 GN PRE-C/CORE.
 OS HEPATITIS B VIRUS.
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT LICHENI-1'85;
 RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
 RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AYW4;
 RA PLUCIENNICZAK A.;
 RL SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 81012091.
 RA GALLIBERT F., MANDART E., FITOUSSI F., TIOLLAIS P., CHARNAY P.;
 "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)
 cloned in E. coli.";
 RL NATURE 281:646-650(1979).
 [4]
 RP SEQUENCE FROM N.A.
 RA BORISOVA G.P., PUMPER P.P., BYCHKO V.V., PUSHKO P.M., KALIS Y.V.,
 RA DISHLER A.V., GREN E.Y., TSIBINGIN V.V., KURAIN R.A.;
 RL DOCL. BIOCHEM. 279:386-390(1985).
 DR EMBL: X85290; G736116; -;
 DR EMBL: X85300; G736152; -;
 DR EMBL: X85313; G736196; -;
 DR EMBL: X85283; G736090; -;
 DR EMBL: X85306; G736174; -;
 DR EMBL: X85716; G527437; -;
 DR EMBL: J02203; G329642; -;
 DR EMBL: X85312; G736193; -;
 DR PFAM: PF00906; Hepatitis_core; 1.
 KW STGNAL.
 SQ SEQUENCE 212 AA; 24350 KM; 71EA2C82 CRC32;

Query Match 46.2%; Score 1375; DB 14; Length 212;
 Best Local Similarity 99.5%; Pred. No. 2.16e-231;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAI 88
 :|||||
 QY 213 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAI 272
 :|||||

DB 89 LCWGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLFHISCLTFGRETIVIEL 148
 :|||||
 QY 273 LCWGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLFHISCLTFGRETIVIEL 332
 :|||||

DB 149 VSEGVWIRTPPAPRNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQSR 208
 :|||||
 QY 333 VSEGVWIRTPPAPRNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQSR 392
 :|||||

DB 209 ESQC 212
 :|||||
 QY 393 ESQC 396

RESULT 2
 ID 068020 PRELIMINARY; PRT: 212 AA.
 AC 068020;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PRE-C/CORE.
 GN HEPATITIS B VIRUS.
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-PATIENT CASTAG-1'85;
 RA LAI M.E., MAZOLENTI A.P., PORRU A., BALESTRIERI A.;
 RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: X85281; G736119; -;
 DR PFAM: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 212 AA; 24336 MW; E0E4C243 CRC32;

Query Match 46.2%; Score 1374; DB 14; Length 212;
 Best Local Similarity 98.9%; Pred. No. 3.37e-231;
 Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAI 88
 :|||||
 QY 213 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAI 272
 :|||||

DB 89 LCWGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLFHISCLTFGRETIVIEL 148
 :|||||
 QY 273 LCWGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLFHISCLTFGRETIVIEL 332
 :|||||

DB 149 VSEGVWIRTPPAPRNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQSR 208
 :|||||
 QY 333 VSEGVWIRTPPAPRNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQSR 392
 :|||||

DB 209 ESQC 212
 :|||||
 QY 393 ESQC 396

RESULT 3
 ID 089597 PRELIMINARY; PRT: 212 AA.
 AC 089597;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HBCAG.
 OC HEPATITIS B VIRUS.
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SUB-TYPE AYW;

Query Match 46.2%; Score 1374; DB 14; Length 212;
 Best Local Similarity 98.9%; Pred. No. 3.37e-231;
 Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAI 88
 :|||||
 QY 213 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAI 272
 :|||||

DB 89 LCWGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLFHISCLTFGRETIVIEL 148
 :|||||
 QY 273 LCWGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLFHISCLTFGRETIVIEL 332
 :|||||

DB 149 VSEGVWIRTPPAPRNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQSR 208
 :|||||
 QY 333 VSEGVWIRTPPAPRNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQSR 392
 :|||||

DB 209 ESQC 212
 :|||||
 QY 393 ESQC 396

RESULT 4
 ID 089437 PRELIMINARY; PRT: 183 AA.
 AC 089437;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE X, PREC AND C GENES (CASTA 2).
 GN CORE.
 OS HEPATITIS B VIRUS.
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT CASTA-2'87;
 RC LAI M.E., MAZOLENTI A.P., PORRU A., BALESTRIERI A.;
 RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: X85289; G736113; -;
 DR PFAM: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 183 AA; 21102 MW; 0C504D47 CRC32;

Query Match 46.1%; Score 1373; DB 14; Length 183;

RX MEDLINE: 94079539.
 RA PREISLER-ADAMS S., SCHLAYER M.J., PETERS T., HETTLER F., GEROK W.,
 RA RASINACK J.;
 RT "Sequence analysis of hepatitis B virus DNA in immunologically
 RT negative infection";
 RL ARCH. VIROL. 133:385-396(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AYW;
 RA KARAYIANNIS P.;
 RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AYW;
 RA KARAYIANNIS P.;
 RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: X72702; G288930; -;
 DR EMBL: X80925; E198084; -;
 DR PFAM: PF00906; Hepatitis_core; 1.
 SQ SEQUENCE 212 AA; 24336 MW; 575D20BF CRC32;


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OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LICHERI-2/87;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85314; G736204; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 183 AA; 21102 MW; 6F38AA3B CRC32;

Query Match
Best Local Similarity 98.4%; Score 1370; DB 14; Length 183;
Matches 180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 60
QY 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 60
Db 61 CAGDMLTATWGVNLEDPASRDLVSYVNTNMGKLFROLIMFHSCLTGTGRTVIEYL 120
QY 61 CAGDMLTATWGVNLEDPASRDLVSYVNTNMGKLFROLIMFHSCLTGTGRTVIEYL 120
Db 121 SEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
QY 121 SEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
Db 181 SOC 183
QY 181 SOC 183

RESULT 9
ID 068068 PRELIMINARY; PRT: 212 AA.
AC 068068;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LICHERI-3/90;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85315; G736207; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24366 MW; AB227A9B CRC32;

Query Match
Best Local Similarity 98.9%; Score 1370; DB 14; Length 212;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 88
QY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 272
Db 89 LCGELMTLATWGVNLEDPASRDLVSYVNTNMGKLFROLIMFHSCLTGTGRTVIEYL 148
QY 273 LCGELMTLATWGVNLEDPASRDLVSYVNTNMGKLFROLIMFHSCLTGTGRTVIEYL 332
Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 333 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 392
Db 209 ESQC 212
QY 393 ESQC 396

RESULT 10
ID 068025 PRELIMINARY; PRT: 212 AA.
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AC 068025;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTAG/3;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85293; G736126; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;

Query Match
Best Local Similarity 98.9%; Score 1370; DB 14; Length 212;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 88
QY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 272
Db 89 LCGELMTLATWGVNLEDPASRDLVSYVNTNMGKLFROLIMFHSCLTGTGRTVIEYL 148
QY 273 LCGELMTLATWGVNLEDPASRDLVSYVNTNMGKLFROLIMFHSCLTGTGRTVIEYL 332
Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 333 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 392
Db 209 ESQC 212
QY 393 ESQC 396

RESULT 11
ID 067872 PRELIMINARY; PRT: 212 AA.
AC 067872;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT C, HBSAG POSITIVE, HBV SUBTYPE ATW;
RA LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A., PORRU A.;
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65257; G59431; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24368 MW; A6BD9DA1 CRC32;

Query Match
Best Local Similarity 98.4%; Score 1369; DB 14; Length 212;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 88
QY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 272
Db 89 LCGELMTLATWGVNLEDPASRDLVSYVNTNMGKLFROLIMFHSCLTGTGRTVIEYL 148
QY 273 LCGELMTLATWGVNLEDPASRDLVSYVNTNMGKLFROLIMFHSCLTGTGRTVIEYL 332
Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 333 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 392
Db 209 ESQC 212
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OY 393 ESQC 396

RESULT 12
ID 067984 PRELIMINARY: PRT: 212 AA.

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT VITTORINA'92;

RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: X85256; G736052; -
DR PFAM: PF00906; Hepatitis_core: 1.

SO SEQUENCE 212 AA; 24322 MM; 83D9780B CRC32;

Query Match 46.0%; Score 1369; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 3,11e-230;

Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 272

DB 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88

OY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 272

DB 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTFGRETVIEYL 148

OY 273 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTFGRETVIEYL 332

DB 149 VSGFWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSQSPRRRSOSR 208

OY 333 VSGFWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSQSPRRRSOSR 392

DB 209 ESQC 212

OY 393 ESQC 396

RESULT 13
ID 068032 PRELIMINARY: PRT: 212 AA.

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CHICHINE-2'86;

RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: X85256; G736139; -
DR PFAM: PF00906; Hepatitis_core: 1.

SO SEQUENCE 212 AA; 24308 MM; 69D87B53 CRC32;

Query Match 46.0%; Score 1369; DB 14; Length 212;
Best Local Similarity 98.4%; Pred. No. 3,11e-230;

Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88

OY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 272

DB 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTFGRETVIEYL 148

OY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 272

DB 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTFGRETVIEYL 148

OY 273 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTFGRETVIEYL 332

DB 149 VSGFWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSQSPRRRSOSR 208

OY 333 VSGFWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSQSPRRRSOSR 392

DB 209 ESQC 212

OY 393 ESQC 396

RESULT 14
ID 068010 PRELIMINARY: PRT: 212 AA.

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT FERRACUTI-2'90;

RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: X85285; G736100; -
DR PFAM: PF00906; Hepatitis_core: 1.

SO SEQUENCE 212 AA; 24292 MM; 04A4D12D CRC32;

Query Match 46.0%; Score 1368; DB 14; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.85e-230;

Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 272

DB 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88

OY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 272

DB 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTFGRETVIEYL 148

OY 273 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTFGRETVIEYL 332

DB 149 VSGFWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSQSPRRRSOSR 208

OY 333 VSGFWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSQSPRRRSOSR 392

DB 209 ESQC 212

OY 393 ESQC 396

RESULT 15
ID 068070 PRELIMINARY: PRT: 212 AA.

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT GORDO/84;

RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: X85316; G736210; -
DR PFAM: PF00906; Hepatitis_core: 1.

SO SEQUENCE 212 AA; 24376 MM; 80F52D0F CRC32;

Query Match 45.9%; Score 1366; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.18e-229;

Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTFGRETVIEYL 148

OY 213 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 272

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Db      29 GMDIDPYKEFGAIVELLISFLPSDFPSPVRDLDLTASALYREALESPHCSPHHTALRQAI 88
QY      213 SMDIDPYKEFGAIVELLISFLPSDFPSPVRDLDLTASALYREALESPHCSPHHTALRQAI 272
Db      89 LCWGEIMTLATWGVNLEDPASRDLYVSYVNTNMGKLFROLMFHISCLTFGRETVEYL 148
QY      273 LCWGEIMTLATWGVNLEDPASRDLYVSYVNTNMGKLFROLMFHISCLTFGRETVEYL 332
Db      149 VSEGVWIRTPPAYRPPNAPILLLTLETTVVRRGRSPRRRTPSPPRRRSQSPRRRSQSR 208
QY      333 VSEGVWIRTPPAYRPPNAPILLLTLETTVVRRGRSPRRRTPSPPRRRSQSPRRRSQSR 392
Db      209 ESQC 212
QY      393 ESQC 396

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Search completed: Thu Dec 16 12:52:36 1999
 Job time : 139 secs.

US3835-1-38183
MDIDPKKEFGATVELLSFLPSDFPSPYRDLDLTASEIITRDGELLQMDFFPEHLVDLQSLMDIDP
YKEFGATVELLSFLPSDFPSPYRDLDLTASEIITRDGELLQMDFFPEHLVDLQSLMDIDP
LEDPSARDLVSVYNTNMGLKFRQLMFIHISCLTFGRETVEYLVSGVWIRTPPAYRPPNAPILSTLPE
TIVRRRGSRPRRTTSPRRRSQSPRRRSQSRQSC1

US 3835-1-38183
Seq 38 residue 1-35
Seq 38 residue 1-183
Seq 1-183 not 30 translation

(TM)

Distribution rights by Oxford Molecular Ltd

Maspar time 11.85 Seconds

ot generated.

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1 MDIDPYKEGATVELLSFLP.....RRRSQSPRRRSQSRRESQC 248
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Gap 11

170751 seqs, 21266608 residues

Listing first 45 summaries

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airt39

Mean 33.490; Variance 173.849; scale 0.193

ived by analysis of the total score distribution

SUMMARIES

72.0	183	13	R68868	Hepatitis B virus pol	2.26e-96
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45	1258	67.9	183	17	R98884	Hepatitis B virus E a	3.75e-90
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ALIGNMENTS

RESULT	1
ID	W50242 standard; Protein: 194 AA.
AC	W50242;
DT	26-SEP-1998 (first entry)
DE	Hepatitis B virus precore p22 polypeptide Met-p22.
KM	Viral replication; inhibitor; HBV; nucleocapsid; gene therapy:
KW	hepatocyte; liver; Met-p22.
OS	Hepatitis B virus.
OS	Synthetic.
FH	Key
FT	Location/Qualifiers
FT	2..194
FT	/label= p22
PN	W09809649-A1.
PD	12-MAR-1998.
PF	03-SEP-1997; 015500.
PR	03-SEP-1996; US-025370.
PA	(GEHO) GEN HOSPITAL CORP.
PI	Melegari M, Scaglioni PP, Wands JR;
DR	WIR; 98-193325/17.
PT	DNA encoding proteins which can be incorporated with wild type
PT	nucleocapsid subunit(s) into a viral nucleocapsid - useful for
PT	inhibition of viral replication, especially hepatitis B virus
PS	Claim 11: Page 40; 60pp; English.
CC	This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
CC	protein with an added N-terminal Met residue. p22 is produced by
CC	elimination of the 19-amino acid leader peptide from the 25 kDa
CC	full-length HBV precore protein (see W50250). Evidence is provided
CC	that HBV replication is inhibited in the presence of high levels of
CC	HBV precore or precore-related proteins. These proteins can be
CC	incorporated into HBV nucleocapsids along with the p21 core protein
CC	(see W50251), which is the usual nucleocapsid component, and
CC	thereby render the nucleocapsids deficient in encapsidating HBV
CC	pregenomic RNA. Thus, over-expression of the precore proteins, or
CC	certain variants of them, leads to transdominant inhibition of HBV
CC	replication. Suitable inhibitory proteins include p25 (see W50250),
CC	p22, Met-p22, p18 (see W50236), Met-p18 (see W50237) and Met-p18-Hee
CC	(see W50238). Heterologous peptides (see W50244-49) may be
CC	inserted into the p22 and Met-p22 polypeptides. The inhibitory
CC	proteins can be produced by recombinant methods using cloned
CC	expression vectors and host cells. They can be provided exogenously

to the target cells for use in inhibiting HBV replication.
 CC Alternatively, a nucleic acid construct that directs overexpression
 CC of an inhibitory protein in target cells is used for the gene
 CC therapy of HBV infection.
 SQ Sequence 194 AA;

Query Match 74.2%; Score 1375; DB 32; Length 194;

Best Local Similarity 99.5%; Pred. No. 9,896-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 gmdidpykxkfegatvellsfipdsfipsvrdlildtasalyrealsepshcphthalrgai 70
 QY 65 SMDIDPKKEGATVELLSFIPDSFIPSVRDLDLDRASALYREALSEPSCPHHTALRQAI 124
 Db 71 lcwgelmtlatwgvnledpasrdlvsyvtntmgjkfrqllwfhiscitfgretvieyl 130
 QY 125 LCWGEMLTATWGVNLEDPASRDLYVSYVNTNMGKFRQLMFHISCLTFRGRETVEYL 184
 Db 131 vsfgvwlrtppayrpnpnaillstlpettvtvrrrgsprrrtsprrrrsgprrrrsgsr 190
 QY 185 VSFGVWLRTPPAYRPNAPILSTLPETTVVRRRGSPRRRTPSPRRRSQSPRRRSQSR 244
 Db 191 esgc 194
 QY 245 ESQC 248

RESULT

ID W50250 standard; Protein; 212 AA.

AC W50250:
 DT 28-SEP-1998 (first entry)
 DE Hepatitis B virus precore p25 polypeptide.
 KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
 OS Hepatocyte; liver; p25 protein.
 KW Hepatitis B virus.
 PN M09809649-A1.
 PD 12-MAR-1998.
 PF 03-SEP-1997; U15500.
 PR 03-SEP-1996; US-025370.
 PA (GEHO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR;
 DR WPI: 98-193325/17.
 DR DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus
 CS Claim 15; Page 35; 60pp; English.
 CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)
 CC protein that is encoded by the full-length HBV precore gene.
 CC Evidence is provided that HBV replication is inhibited in the
 CC presence of high levels of HBV precore or precore-related proteins.
 CC These proteins can be incorporated into HBV nucleocapsids along
 CC with the p21 core protein (see W50251), which is the usual
 CC nucleocapsid component, and thereby render the nucleocapsids
 CC deficient in encapsidating HBV pregenomic RNA. Thus, over-
 CC expression of the precore proteins, or certain variants of them,
 CC leads to transdominant inhibition of HBV replication. Suitable
 CC inhibitory proteins include p25, p22 (see W50241), Met-p22 (see
 CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
 CC (see W50238). The inhibitory proteins can be produced by
 CC recombinant methods using claimed expression vectors and host
 CC cells. They can be provided exogenously to the target cells for
 CC use in inhibiting HBV replication. Alternatively, a nucleic acid
 CC construct that directs overexpression of an inhibitory protein in
 CC target cells is used for the gene therapy of HBV infection.
 SQ Sequence 212 AA;

Query Match 74.2%; Score 1375; DB 32; Length 212;

Best Local Similarity 99.5%; Pred. No. 9,896-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 gmdidpykxkfegatvellsfipdsfipsvrdlildtasalyrealsepshcphthalrgai 88
 QY 65 SMDIDPKKEGATVELLSFIPDSFIPSVRDLDLDRASALYREALSEPSCPHHTALRQAI 124

Db 89 lcwgelmtlatwgvnledpasrdlvsyvtntmgjkfrqllwfhiscitfgretvieyl 148

QY 125 LCWGEMLTATWGVNLEDPASRDLYVSYVNTNMGKFRQLMFHISCLTFRGRETVEYL 184

Db 149 vsfgvwlrtppayrpnpnaillstlpettvtvrrrgsprrrtsprrrrsgprrrrsgsr 208

QY 185 VSFGVWLRTPPAYRPNAPILSTLPETTVVRRRGSPRRRTPSPRRRSQSPRRRSQSR 244

Db 209 esgc 212

QY 245 ESQC 248

RESULT

ID R27473 standard; Protein; 346 AA.

AC R27473:

DT 24-FEB-1993 (first entry)

DE S12/core protein.

KW Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;

KW vaccinia virus; I3L; promoter; NVVAC; recombinant; HBV L;

KW large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;

KW S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;

KW deletion loci; recipient loci.

OS Synthetic.

PH key Location/Qualifiers

FT region 1..108

FT region /label S1

FT region 109..163

FT region /label S2

FT region 164..346

FT region /label Core

PN W09215672-A.

PD 17-SEP-1992.

PF 09-MAR-1992; U01906.

PR 07-MAR-1991; US-666056.

PR 11-JUN-1991; US-713967.

PR 06-MAR-1992; US-847951.

PA (VIRO-) VIROGENETICS CORP.

PI Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GP,

PI Limbach KJ, Norton EK, Paoletti E, Perkins ME, Pincus SE,

PI Riviere M, Taragaglia J, Taylor J;

DR N-PSDB; Q29105.

PT vaccine comprises recombinant, attenuated pox-virus - use for

PT vaccinating against viral infections such as rabies, hepatitis B,

PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 45pp; English.

CC The sequence given is encoded by an expression cassette which

CC comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/

CC core) which is precisely linked to the 13L promoter derived from

CC vaccinia virus. This DNA sequence was linked to the S1 and S2

CC sequences and this fragment was used in the construction of a NVVAC

CC recombinant expressing the HBV gene. Other HBV genes were also used

CC in the construction. These were HBV M protein (small pre-S antigen,

CC spsAg) and HBV L (large pre-S antigen, lpsAg). Each of these gene

CC sequences were inserted individually into three different sites of

CC NVVAC separated by from each other by large regions of vaccinia DNA

CC containing essential genes. NVVAC is a Copenhagen vaccine strain of

CC vaccinia virus which has been modified by deletion of six non-essential

CC regions of the genome encoding known or potential virulence factors.

CC The deletion loci were engineered as recipient loci for the insertion

CC of foreign genes. The spacing of the three inserted sequences ensured

CC that any recombination that did occur would lead to disruption of the

CC vaccinia genome and would cause unviable vaccinia virus. See also

SQ Q25501-864.

Sequence 346 AA;

Query Match 74.2%; Score 1375; DB 5; Length 346;

Best Local Similarity 99.5%; Pred. No. 9,896-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 163 nmddidpykxkfegatvellsfipdsfipsvrdlildtasalyrealsepshcphthalrgai 222

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QY      :|||||
65  SMDIDPKKEGATVELLSFSDFFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 124
Db      1cvgelmtlatwgvnledpasrdlvsvyvdtnmgkfrqllwfhsicltfgretvleyl 282
QY      125 LCMGELMTLATWGVNLEDPASRDLYVSVYNTNMGKFRQLLMFHISCLTFGRRTVLEYL 184
Db      283 vsfgvwlrtppayrpnapllstlpetlvrrrgsprrrrrsgsprrrrrsgsr 342
QY      185 VSEGVWIRTPPAYRPAPNPILSTLPETTVVRRGRSPRRRTSPRRRRSQSPRRRRSQSR 244
Db      343 esgc 346
QY      245 ESQC 248

RESULT 4
ID      P80959 standard: protein: 184 AA.
AC      P80959;
DE      19-NOV-1990 (first entry)
DT      Hepatitis B virus subtype ayw. core protein.
KM      conjugate: fusion protein; hepatitis B core protein; HBV subtype ayw.;
KW      T cell stimulating polypeptide; vaccines.
OS      Synthetic.
PN      EP-271302-A.
PD      15-JUN-1988.
PF      07-DEC-1987; 310725.
PR      07-OCT-1987; US-106538.
RA      07-OCT-1987; US-939617.
PA      (SCRT-) Scripts Clinic Res.
PI      Thornton GB, Moriarty AM, Milllich DR, McLachlan A.;
DR      WPI: 88-163287/24.
PT      New conjugates and fusion proteins of immunogenic polypeptide -
PT      and hepatitis B core antigen and T cell stimulating polypeptide
PS      corep. to core antigen, useful in vaccines.
CC      disclosure: p: English.
CC      This sequence contains the T cell stimulating epitopes, amino acid
CC      residue 1-55 and 70-140. It is believed that the regions 1-44 and
CC      70-140 do not contain determinants that suppress T cell activation.
CC      Polypeptides essentially consisting of 15 to 55 amino acids
CC      corresponding to the above mentioned HBV regions are T cell
CC      stimulating. Coupling a polypeptide immunogen to such sequences,
CC      e.g. by using a bifunctional reagent which forms a disulphide link,
CC      improves its immunogenicity. These are useful in vaccines and can be used
CC      therapeutically to improve T cell response to HBcAg in infected
CC      subjects.
CC      See also P80896-P80898 and P80951-P80859.
SQ      Sequence 184 AA:

Query Match      73.5%: Score 1363; DB 1; Length 184;
Best Local Similarity 99.5%: Pred. No. 9.52e-99;
Matches 183; Conservative 0; Mismatches 0; Indels 1; Gaps 1:

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DT      28-SEP-1998 (first entry)
DE      Hepatitis B virus precore p22 polypeptide.
KM      Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
KW      hepatocyte; liver; p22 protein.
OS      Hepatitis B virus.
FH      Key      Location/Qualifiers
FT      Region      82..98
FT      WO9809649-A1.
FT      12-MAR-1998.
PD      03-SEP-1997; 015500.
PR      03-SEP-1996; US-025370.
PA      (GEO) GEN HOSPITAL CORP.
PI      Melegari M, Scaglioni PP, Wands JR;
DR      WPI: 98-193325/17.
PT      DNA encoding proteins which can be incorporated with wild type
PT      nucleocapsid subunit(s) into a viral nucleocapsid - useful for
PT      inhibition of viral replication, especially hepatitis B virus
PS      Claim 9; Page 34-35; 60pp: English.
CC      This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
CC      protein that is produced by elimination of the 19-amino acid leader
CC      peptide from the 25 kDa full-length HBV precore protein (see
CC      W50250). Evidence is provided that HBV replication is inhibited in
CC      the presence of high levels of HBV precore or precore-related
CC      proteins. These proteins can be incorporated into HBV nucleocapsids
CC      along with the p21 core protein (see W50251), which is the usual
CC      nucleocapsid component, and thereby render the nucleocapsids
CC      deficient in encapsidating HBV pregenomic RNA. Thus, over-
CC      expression of the precore proteins, or certain variants of them,
CC      leads to transdominant inhibition of HBV replication. Suitable
CC      inhibitory proteins include p25 (see W50250), p22, Met-p22 (see
CC      W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
CC      (see W50238). Heterologous peptides (see W50244-49) may be
CC      inserted into the p22 and Met-p22 polypeptides. The inhibitory
CC      proteins can be produced by recombinant methods using claimed
CC      expression vectors and host cells. They can be provided exogenously
CC      to the target cells for use in inhibiting HBV replication.
CC      Alternatively, a nucleic acid construct that directs overexpression
CC      of an inhibitory protein in target cells is used for the gene
CC      therapy of HBV infection.
SQ      Sequence 193 AA:

Query Match      73.3%: Score 1359; DB 32; Length 193;
Best Local Similarity 98.4%: Pred. No. 2.02e-98;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0:

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FT /note- "immunodominant region"
 PN WO9809649-A1.
 PD 12-MAR-1998.
 PR 03-SEP-1997; U15500.
 PR 03-SEP-1996; US-025370.
 PA (GENO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR;
 DR WPI: 98-193325/17.
 PR DNA encoding proteins which can be incorporated with wild type
 PR nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PR inhibition of viral replication, especially hepatitis B virus
 PS Disclosure: Page 41-42; 60pp; English.
 CC This is the 21 kDa (p21) protein of hepatitis B virus (HBV) that
 CC assembled into a 180 kDa subunit nucleocapsid structure that
 CC promotes viral replication. Evidence is provided that HBV
 CC replication is inhibited in the presence of high levels of HBV
 CC precore or precore-related proteins. These proteins can be
 CC incorporated into HBV nucleocapsids along with the p21 core protein
 CC and thereby render the nucleocapsids deficient in encapsidating HBV
 CC pregenomic RNA. Thus, over-expression of the precore proteins or
 CC certain variants of them, leads to transdominant inhibition of HBV
 CC replication. Suitable inhibitory proteins include p25 (see
 CC W50250), p22 (see W50241), Met-p22 (see W50242), p18 (see W50235),
 CC Met-p18 (see W50237) and Met-p18-Het (see W50238). These proteins
 CC can be produced by recombinant methods using claimed expression
 CC vectors and host cells, and can be provided exogenously to target
 CC cells for use in inhibiting HBV replication. Alternatively, a
 CC nucleic acid construct that directs overexpression of an inhibitory
 CC protein in target cells is used for the gene therapy of HBV
 CC infection.
 S0 Sequence 183 AA:

Query Match 73.2%; Score 1358; DB 32; Length 183;
 Best Local Similarity 98.9%; Pred. No. 2,44e-98;
 Matches 181; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 mdidpykefgatvelslsfpsdfsvrdlldtasalyrealesphesphhtalrgall 60
 QY 66 MDIDPYKEFGATVELSLSPDSDFPSVRDLDTASALYREALESPEHCSPHHTALRQAIL 125
 DB 61 cweelmtlatwgvnlledpasrdlvsvyvtmglkftrqlwfhscldfgetvleylv 120
 QY 126 CWGELMTLATWGVNLLEDPASRDLVSVYVTNMGKLFQRLMFHISCLFGEETVLEYLV 185
 DB 121 sfqgvvltppayrppnapilslpetvtvrrgrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr 180
 QY 186 SFGVWIRPPAYRPPNAPILSLPETVTVRRGRSPRRRRTPSPRRRRSOSPRRRRSQSR 245
 DB 181 sgc 183
 QY 246 SOC 248
 OS Hepatitis B virus.
 KW core protein; replication; antiviral; gene therapy.
 FH Hepatitis B virus.
 FH Key
 FT Location/Qualifiers
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 71-180 in mutant
 FT polypeptides of the invention (Claim 23)"
 FT misc_difference 81..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 81 and 180 in mutant
 FT polypeptides of the invention (Claim 5)"
 FT misc_difference 171..180
 FT /note= "C-terminus of core protein is at any amino

FT acid position between 171 and 180 in mutant
 FT polypeptides of the invention (Claim 6)"
 FT misc_difference 174..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 174 and 180 in mutant
 FT polypeptides of the invention (Claim 26)"
 FT misc_difference 178
 FT /note= "C-terminus of core protein is at amino acid
 FT position 178 in mutant polypeptides of the
 FT invention (Claim 7)"
 FT misc_difference 178
 FT /note= "C-terminus of core protein is at amino acid
 FT position 178 in mutant polypeptides of the
 FT invention (Claim 7)"
 FT misc_difference 172..183
 FT /note= "amino acid residues 172-183, pref. 174-180,
 FT are deleted from the core protein in mutant
 FT polypeptides of the invention"

PN WO9700698-A1.
 PD 09-JAN-1997.
 PR 20-JUN-1996; U10602.
 PR 20-JUN-1995; US-017814.
 PA (GENO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR;
 DR WPI: 97-087176/08.
 DR N-PSDB: 149594.
 PR New method for inhibiting the replication of hepadnaviruses -
 PR comprises introducing a mutant polypeptide with a mutated core
 PR protein or corresponding nucleic acid, for treating, e.g. hepatitis
 PR B

PS Claim 5; Page 55-56; 83pp; English.
 CC Alteration of the C-terminus of the core protein (W09044) of
 CC hepatitis B virus (HBV) or other hepadnavirus creates a mutant
 CC polypeptide capable of reducing replication of the wild-type virus
 CC by a dominant negative mechanism. The inhibitory effect is
 CC species-specific and is achieved by deletion of a few C-terminal
 CC amino acids from the core protein, and/or by joining the core
 CC protein to a hepadnavirus surface protein (see also W09045),
 CC creating a core-surface fusion. Such mutant polypeptides (see
 CC also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
 CC infection.
 S0 Sequence 183 AA:

Query Match 73.0%; Score 1353; DB 20; Length 183;
 Best Local Similarity 98.9%; Pred. No. 6,28e-98;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 mdidpykefgatvelslsfpsdfsvrdlldtasalyrealesphesphhtalrgall 60
 QY 66 MDIDPYKEFGATVELSLSPDSDFPSVRDLDTASALYREALESPEHCSPHHTALRQAIL 125
 DB 61 cweelmtlatwgvnlledpasrdlvsvyvtmglkftrqlwfhscldfgetvleylv 120
 QY 126 CWGELMTLATWGVNLLEDPASRDLVSVYVTNMGKLFQRLMFHISCLFGEETVLEYLV 185
 DB 121 sfqgvvltppayrppnapilslpetvtvrrgrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr 180
 QY 186 SFGVWIRPPAYRPPNAPILSLPETVTVRRGRSPRRRRTPSPRRRRSOSPRRRRSQSR 245
 DB 181 sgc 183
 QY 246 SOC 248
 OS Hepatitis B virus.
 KW core protein; replication; antiviral; gene therapy.
 FH Hepatitis B virus.
 FH Key
 FT Location/Qualifiers
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 71-180 in mutant
 FT polypeptides of the invention (Claim 23)"
 FT misc_difference 81..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 81 and 180 in mutant
 FT polypeptides of the invention (Claim 5)"
 FT misc_difference 171..180
 FT /note= "C-terminus of core protein is at any amino

RESULT 8
 ID R05635 standard; protein; 183 AA.
 AC R05635.
 DT 30-OCT-1990 (first entry)
 DE Hepatitis B antigen.
 KW Hepatitis B virus; vaccine; HBV; ds.
 OS Synthetic.
 PN EP-374869-A.
 PD 27-JUN-1990.

PF 1-JAN-1989; 123526.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOJ) Biogen Inc.
PI Murray K, Schaller HE;
DR WPI: 90-195067/26.
DR N-PSDB: Q04799.
PT Recombinant DNA encoding Hepatitis B virus polypeptide antigens -
used in detection of infection and in vaccine prodn.
PS Disclosure: 4pp: English.
CC Polypeptide fragments encoded by the DNA sequence are antigenic for
CC HBV and may be used as a vaccine or in detection. Peptides may be
CC cultured in a suitable bacterial host such as E.coli.
CC Fragments of the sequence are also claimed as being antigenically
CC useful.
SQ Sequence 183 AA;

Query Match 72.8%; Score 1349; DB 1; Length 183;
Best Local Similarity 96.7%; Pred. No. 1.33e-97;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdidykefgatvellstfspdffpsvrdlldtaaalrydalespeshphltalrgall 60
|||||
QY 66 MDIDYKEFGATVELLSPLSPDFPSVRLDLDTASALYREALSEPHSPHTALRQAIL 125
|||||
Db 61 cwgdlmtatwgvnlledpasrdlvsvyntnmgkrfqlwfhfscitfgretyleyiv 120
|||||
QY 126 CWGELMTATWGVNLLEDPASRDLVSVYNTNMGKRFQLWFMHISCLTFGRETYIELYV 185
|||||
Db 121 sfgywlrtpayrpnpadlsltpetvrrrgsprrrrrsqsprrrrsqr 180
|||||
QY 186 SFGWIRTPAYRPNPADILSTPETVRRRGSPRRRTPSPRRRSQSPRRRSQSR 245
|||||
Db 181 sqc 183
|||
QY 246 SQC 248

RESULT 9
ID P00041 standard; Protein; 183 AA.
AC P00041: 1992 (first entry)
DE Sequence of core antigen.
KW Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
OS Hepatitis B virus.
PN EP--13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979; 303017.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOJ) BIOGEN NV.
PI Murray K, Schaller HE;
DR WPI: 80-57268C/33.
DR N-PSDB: N00003.
PT Recombinant DNA coding for polypeptide - have specificity of
PT hepatitis B viral antigens in detection or antibody stimulation
PS Example: Figs 3-4: 43pp: English.
CC Human serum from a single HBsAg positive, HBeAg positive donor
CC (serotype adyM) was used to prep. a DNA-contg. pellet which was
CC labelled with 3H or 32P as described by P. M. Kaplan et al (1973).
CC The labelled DNA was then extracted with phenol from the resulting
CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
CC It was then cloned in plasmid pBR322 which was used to transform E.
CC coli. Micro-organisms prepd. by the processes are deposited at the
CC NCIB as pBR322-HBV-6-L, e.g. E. coli HB101/pBR322-Pst I dg;
CC HBV-Kpn I dc; Tetr Amps HBV+.
SQ Sequence 183 AA;

Query Match 72.8%; Score 1349; DB 5; Length 183;
Best Local Similarity 96.7%; Pred. No. 1.33e-97;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdidykefgatvellstfspdffpsvrdlldtaaalrydalespeshphltalrgall 60
|||||
QY 66 MDIDYKEFGATVELLSPLSPDFPSVRLDLDTASALYREALSEPHSPHTALRQAIL 125
|||||
Db 61 cwgdlmtatwgvnlledpasrdlvsvyntnmgkrfqlwfhfscitfgretyleyiv 120
|||||
QY 126 CWGELMTATWGVNLLEDPASRDLVSVYNTNMGKRFQLWFMHISCLTFGRETYIELYV 185
|||||
Db 121 sfgywlrtpayrpnpadlsltpetvrrrgsprrrrrsqsprrrrsqr 180
|||||
QY 186 SFGWIRTPAYRPNPADILSTPETVRRRGSPRRRTPSPRRRSQSPRRRSQSR 245
|||||
Db 181 sqc 183
|||
QY 246 SQC 248

RESULT 10
ID W09048 standard; Protein; 397 AA.
AC W09048:
DE Plasmid pHBV DN AA encoded HBV dominant negative polypeptide.
DE Hepadnavirus; woodchuck hepatitis virus; hepatitis delta virus;
KW HBV; ground squirrel hepatitis B virus; duck hepatitis B virus;
KW core protein; replication; antiviral; gene therapy; pHBV DN AA.
OS Hepatitis B virus.
FS Key
FT Location/Qualifiers
FT 1..179
FT /label= HBV_core
FT /note= "positions 1-179 correspond to amino acids
FT 1-179 of HBV core protein"
FT 180..397
FT /note= "positions 180-397 correspond to amino
FT acids 9-226 of HBV surface protein"
FN W09700698-A1.
PD 09-JAN-1997.
PF 20-JUN-1996; U10602.
PR 20-JUN-1995; US-017814.
PA (GENO) GEN HOSPITAL CORP.
PI Melegari M, Scaglioni PP, Wands JR;
DR WPI: 97-087176/08.
DR N-PSDB: T49598.
PT New method for inhibiting the replication of hepadnaviruses -
PT comprises introducing a mutant polypeptide with a mutated core
PT protein or corresponding nucleic acid, for treating, e.g. hepatitis
PT B
PS Disclosure: Page 46-48; 83pp: English.
CC Plasmid pHBV DN AA carries an insert (T49598) coding for a protein
CC (W09048) comprising a hepatitis B virus (HBV) core protein (see
CC also W09044) fused in-frame at amino acid 179 with the HBV surface
CC protein (see also W09045) at amino acid 8. Plasmid pHBV DN BB
CC (T49599) expresses the HBV core fused at amino acid 175 to the
CC surface protein at amino acid 112 (W09049). pHBV DN AA was at
CC least as potent an inhibitor of HBV replication as construct
CC pHBV DN (T49597). pHBV DN BB was less inhibitory than pHBV DN.
CC Vectors expressing hepadnavirus dominant negative core mutants can
CC be utilised in the gene therapy of viral infections.
SQ Sequence 397 AA;

Query Match 72.5%; Score 1344; DB 20; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.43e-97;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mdidykefgatvellstfspdffpsvrdlldtaaalrydalespeshphltalrgall 60
|||||
QY 66 MDIDYKEFGATVELLSPLSPDFPSVRLDLDTASALYREALSEPHSPHTALRQAIL 125
|||||
Db 61 cwgdlmtatwgvnlledpasrdlvsvyntnmgkrfqlwfhfscitfgretyleyiv 120
|||||
QY 126 CWGELMTATWGVNLLEDPASRDLVSVYNTNMGKRFQLWFMHISCLTFGRETYIELYV 185
|||||
Db 121 sfgywlrtpayrpnpadlsltpetvrrrgsprrrrrsqsprrrrsqr 179

Query 186 SFGVWIRTPPAYRPNPAPILSTLPEITVVRGRGSRPRRTSPSPRRRSOSR 244

RESULT 11
ID P00004 standard: Protein; 184 AA.

AC P00004;
DT 14-OCT-1992 (first entry)
DE Sequence of core antigen.
KM Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
OS Hepatitis B virus.

PN EP-13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979; 303017.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOU) BIOGEN NV.
PI Murray K, Schaller HE;
DR WPI; 80-57268C/33.
N-PSDB: N00002.

PT Recombinant DNA coding for polypeptide - have specificity of
hepatitis B viral antigens in detection or antibody stimulation
PS Claim 13; Page 40; 43pp; English.

CC Human serum from a single HBsAg positive, HBeAg positive donor
(serotype adym) was used to prep. a DNA-contg. pellet which was
labelled with 3H or 32P as described by P. M. Kaplan et al (1973).

CC The labelled DNA was then extracted with phenol from the resulting
CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).

CC It was then cloned in plasmid pBR322 which was used to transform E.
CC coli. Micro-organisms prepd. by the processes are deposited at the
CC NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dg:

CC HBV-Kpn I dc: Tetr Amps HBV+.
SO Sequence 184 AA;

Query Match 72.2%; Score 1338; DB 5; Length 184;

Best Local Similarity 96.2%; Pred. No. 1,06e-96;
Matches 177; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

Db 1 mdidpykefgatvellsfipdsdfpsvcrdlidtaaalaydalespeshphthalrgai 60

Qy 66 MDIDPYKEFGATVELLSLPSDFPSV-RDLDTASALYREALSPESHPHHTALRQAI 124

Db 61 lwcgdlmtlatwgnledpasrdlvsyvnmgikrlqlwfhiscitfgretvleyl 120

Qy 125 LCMGELMTLATWGVNLEDPASRDLVSYVNTMNGKLFRLMFHISCLTFRGRETVEYL 184

Db 121 vsfgvwlrtppayrpnpapilstlpettvrrrgsrprrrrsosprrrrsosqr 180

Qy 185 VSFGVWLRTPPAYRPNPAPILSTLPEITVVRGRGSRPRRTSPSPRRRSOSR 244

Db 181 esgc 184

Qy 245 ESQC 248

RESULT 12
ID R40806 standard: Protein; 196 AA.

AC R40806;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 fusion.
KM Hepatitis B core; HBC; PV-1; IL-1 beta; Interleukin; plasmid.
OS Synthetic.

FN Key Location/Qualifiers
FT region 7..13
FT protein /label= PV-1
FT 14..196
FT /label= HBC

PN J05192170-A.

PD 03-AUG-1993.

PF 24-SEP-1991; 243800.

PR 24-SEP-1991; JP-243800.

PA (NISW) NISSHIN OIL MILLS LTD.

DR WPI; 93-277479/35.

DR N-PSDB: Q47736.

PT Recombinant plasmid for high immunogenicity virus - contains
recombined haemagglutinin gene, hepatitis B core gene of vaccinia
virus and exotic genes

PS Disclosure; Fig 7, 12pp; Japanese.

CC The hepatitis B core gene is recombined with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.

SO Sequence 196 AA;

Query Match 72.1%; Score 1336; DB 8; Length 196;

Best Local Similarity 95.1%; Pred. No. 1.55e-96;
Matches 175; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Db 13 amdidpykefgasvellsfipdsdfpsvcrdlidtaaalaydalespeshphthalrgai 72

Qy 65 SMDIDPYKEFGATVELLSLPSDFPSV-RDLDTASALYREALSPESHPHHTALRQAI 124

Db 73 lwcgdlmtlatwgnledpasrdlvsyvnmgikrlqlwfhiscitfgretvleyl 132

Qy 125 LCMGELMTLATWGVNLEDPASRDLVSYVNTMNGKLFRLMFHISCLTFRGRETVEYL 184

Db 133 vsfgvwlrtppayrpnpapilstlpettvrrrgsrprrrrsosprrrrsosqr 192

Qy 185 VSFGVWLRTPPAYRPNPAPILSTLPEITVVRGRGSRPRRTSPSPRRRSOSR 244

Db 193 esgc 196

Qy 245 ESQC 248

RESULT 13
ID R40806 standard: Protein; 208 AA.

AC R40806;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 / IL-1 fusion.

KM Hepatitis B core; HBC; PV-1; IL-1 beta; Interleukin; plasmid.
OS Synthetic.

FN Key Location/Qualifiers
FT region 8..19
FT region /label= PV-1
FT 20..25
FT /label= IL-1
FT 26..208
FT protein /label= HBC

PN J05192170-A.

PD 03-AUG-1993.

PF 24-SEP-1991; 243800.

PR 24-SEP-1991; JP-243800.

PA (NISW) NISSHIN OIL MILLS LTD.

DR WPI; 93-277479/35.

DR N-PSDB: Q47738.

PT Recombinant plasmid for high immunogenicity virus - contains
recombined haemagglutinin gene, hepatitis B core gene of vaccinia
virus and exotic genes

PS Disclosure; Fig 9; 12pp; Japanese.

CC The hepatitis B core gene is recombined with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.

SO Sequence 208 AA;

Query Match 72.1%; Score 1337; DB 8; Length 208;

Best Local Similarity 94.6%; Pred. No. 1.28e-96;
Matches 175; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Db 24 lgnmidpykefgasvellsfipdsdfpsvcrdlidtaaalaydalespeshphthalrga 83

Qy 64 LSNMIDPYKEFGATVELLSLPSDFPSV-RDLDTASALYREALSPESHPHHTALRQAI 123

Db 84 lwcgdlmtlatwgnledpasrdlvsyvnmgikrlqlwfhiscitfgretvleyl 143

```

OY 124 ILICWELMTLATWGVNLEDPASRDLVSVYNTNMGKRFQLMHISCLTGRETVLEY 183
DB 144 LVSFGVWIRTPPAYRPPNAPILSTLPETTVRRRGSRPRRRRSQSPRRRSQS 203
OY 184 LVSFGVWIRTPPAYRPPNAPILSTLPETTVRRRGSRPRRRRSQSPRRRSQS 243
DB 204 resqc 208
OY 244 RESQC 248

```

```

RESULT 14
ID P40311 standard; Protein: 183 AA.
AC P40311.
DT 18-AUG-1992 (first entry)
DE Hepatitis virus core antigen.
KW HBCAG; vaccine; diagnosis; HBV infection.
OS Hepatitis B virus.
PN J59074985-A.
PD 27-APR-1984.
PF 19-OCT-1982; 183432.
PR 19-OCT-1982; JP-183432.
PA (TAKE ) TAKEDA CHEMICAL IND KK.
DR MPI: 84-143231/23.
PT DNA used in prevention of infections by hepatitis virus B -
  comprises structural gene of hepatitis virus adr B surface antigen
  coding gene and at least 1 virus core antigen structural gene.
PS Disclosure: Fig 3; 13pp; Japanese.
CC The sequence is that of hepatitis virus core antigen (HBCAG). It
  can be used as a vaccine for the prevention of infections by
  hepatitis B virus (HBV) and also in the diagnosis of early stages
  of HBV infection. See also P40310.
SQ Sequence 183 AA:

```

```

Query Match 72.0%; Score 1334; DB 4; Length 183;
Best Local Similarity 95.6%; Pred. No. 2,266-96;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

DB 1 mdidpykefgasvvelsfpsdfpsirdldtasalyrealsephecsphhtalrgall 60
OY 66 MDIDPYKEGATVELLSFSPDFPSVRDLDTASALYREALSEPHECSPHHTALRQAIL 125
OY 126 CWGEIMTLATWGVNLEDPASRDLVSVYNTNMGKRFQLMHISCLTGRETVLEYLV 185
DB 121 sfgvwlrtppayrppnapilstlpetvrrrgsrprrrrsqsprrrrsqsre 180
OY 186 SFGVWIRTPPAYRPPNAPILSTLPETTVRRRGSRPRRRRSQSPRRRSQSRE 245
DB 181 sqc 183
OY 246 SOC 248

```

```

RESULT 15
ID R40805 standard; Protein: 183 AA.
AC R40805.
DT 16-FEB-1994 (first entry)
DE Hepatitis B core protein.
KW Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Hepatitis B virus.
PN J05192170-A.
PD 03-AUG-1993.
PR 24-SEP-1991; 243800.
PA (NISW ) NISSHIN OIL MILLS LTD.
DR MPI: 93-277479/35.
PT Recombinant plasmid for high immunogenicity virus - contains
  recombinant haemagglutinin gene, hepatitis B core gene of vaccinia
  virus and exotic genes

```

```

PS Disclosure: Fig 6; 12pp; Japanese.
CC The hepatitis B core gene is recombinated with PV-1 DNA
  and IL-1 beta to form a plasmid (Q47738) which is then used to produce
  a vaccine. NB: Sequence is difficult to read in the original
  specification.
SQ Sequence 183 AA:

```

```

Query Match 72.0%; Score 1334; DB 8; Length 183;
Best Local Similarity 95.6%; Pred. No. 2,266-96;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

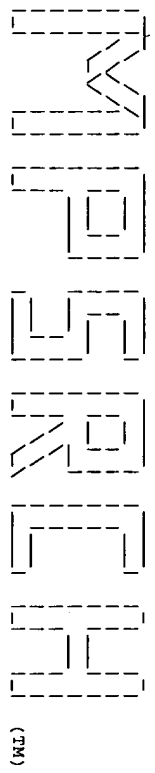
DB 1 mdidpykefgasvvelsfpsdfpsirdldtasalyrealsephecsphhtalrgall 60
OY 66 MDIDPYKEGATVELLSFSPDFPSVRDLDTASALYREALSEPHECSPHHTALRQAIL 125
DB 61 CWGEIMTLATWGVNLEDPASRDLVSVYNTNMGKRFQLMHISCLTGRETVLEYLV 120
OY 126 CWGEIMTLATWGVNLEDPASRDLVSVYNTNMGKRFQLMHISCLTGRETVLEYLV 185
DB 121 sfgvwlrtppayrppnapilstlpetvrrrgsrprrrrsqsprrrrsqsre 180
OY 186 SFGVWIRTPPAYRPPNAPILSTLPETTVRRRGSRPRRRRSQSPRRRSQSRE 245
DB 181 sqc 183
OY 246 SOC 248

```

```

Search completed: Thu Dec 16 13:00:09 1999
Job time : 172 secs.

```

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Msarch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 13:00:27 1999; Maspar time 12.64 Seconds
Tabular output not generated. 786.145 Million cell updates/sec

Title: >US3835-1-38183
Description: (1-248) from us3835-1-38183.pep
Perfect Score: 1854
Sequence: 1 MDIDYKEFGATVLLSFLP.....RRRRSQSPRRRRSQSRNSQC 248

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 47.523; Variance 119.912; scale 0.396

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1375	74.2	212	1	NKVLAH e antigen precursor / 4.43e-199	
2	1373	74.1	183	2	S53207 core antigen - hepati 9.53e-199	
3	1374	74.1	212	2	S53211 e antigen precursor / 6.50e-199	
4	1374	74.1	212	2	S32204 e antigen precursor / 6.50e-199	
5	1373	74.1	212	2	S20750 e antigen precursor / 9.53e-199	
6	1370	73.9	183	2	S53270 core antigen - hepati 3.01e-198	
7	1370	73.9	212	2	S53216 e antigen precursor / 3.01e-198	
8	1370	73.9	212	2	S53272 e antigen precursor / 3.01e-198	
9	1369	73.8	212	2	S53163 e antigen precursor / 4.42e-198	
10	1369	73.8	212	2	S20746 e antigen precursor / 4.42e-198	
11	1369	73.8	212	2	S53225 e antigen precursor / 4.42e-198	
12	1368	73.8	212	2	S53198 e antigen precursor / 6.48e-198	
13	1366	73.7	212	2	S53223 e antigen precursor / 1.39e-197	
14	1366	73.7	212	2	S53274 e antigen precursor / 1.39e-197	
15	1364	73.6	183	2	S53169 core antigen - hepati 3.00e-197	
16	1363	73.5	183	2	S53247 core antigen - hepati 4.40e-197	
17	1363	73.5	212	2	S53202 e antigen precursor / 4.40e-197	
18	1363	73.5	212	2	S53159 e antigen precursor / 4.40e-197	
19	1363	73.5	212	2	S53200 e antigen precursor / 4.40e-197	
20	1362	73.5	212	2	S53251 e antigen precursor / 6.46e-197	
21	1360	73.4	212	2	S53204 e antigen precursor / 1.39e-196	
22	1360	73.4	212	2	S53227 e antigen precursor / 1.39e-196	
23	1359	73.3	212	2	S53253 e antigen precursor / 2.04e-196	

24	1358	73.2	211	1	NKVLAI e antigen precursor / 2.99e-196
25	1357	73.2	212	2	S53281 e antigen precursor / 4.39e-196
26	1355	73.1	212	1	NKVLBI e antigen precursor / 9.44e-196
27	1355	73.1	212	2	S53242 e antigen precursor / 9.44e-196
28	1351	72.9	183	2	S53129 core antigen - hepati 4.37e-195
29	1351	72.9	212	2	S53240 e antigen precursor / 4.37e-195
30	1349	72.8	183	1	NKVLAI core antigen - hepati 9.41e-195
31	1349	72.8	183	2	S53181 core antigen - hepati 9.41e-195
32	1348	72.7	183	2	S53232 core antigen - hepati 1.38e-194
33	1348	72.7	183	2	S53260 core antigen - hepati 1.38e-194
34	1345	72.5	183	2	S53152 core antigen - hepati 1.36e-194
35	1344	72.5	212	2	S53229 e antigen precursor / 6.39e-194
36	1343	72.4	183	2	S53214 core antigen - hepati 9.37e-194
37	1342	72.4	183	2	S53140 core antigen - hepati 1.37e-193
38	1341	72.3	183	2	S53267 core antigen - hepati 2.02e-193
39	1341	72.3	183	2	S53189 core antigen - hepati 2.02e-193
40	1341	72.3	212	2	S53238 e antigen precursor / 2.02e-193
41	1340	72.3	212	2	S53257 e antigen precursor / 2.96e-193
42	1339	72.2	183	2	S53137 core antigen - hepati 4.34e-193
43	1339	72.2	212	2	S25651 e antigen precursor / 4.34e-193
44	1338	72.2	212	2	S53236 e antigen precursor / 6.36e-193
45	1337	72.1	212	1	NKVLJ2 e antigen precursor / 9.33e-193

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE NKVLAH #type complete
e antigen precursor / core antigen - hepatitis B virus
(subtype ayw4, isolate hb321 and others)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal name hepatitis B virus; HBV
#variety subtype ayw4, isolate hb321; isolate patient Ferrucci1'83;
isolate patient Castag'83; isolate patient Sanna'84;
isolate patient Licheri-1'85; isolate patient Flore-1'86;
isolate patient Licheri'83
18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change
10-Oct-1997
DATE S47405; S53191; S53209; S53234; S53264; S53249; S53262;
S53277; A03711
ACCESSIONS
REFERENCE S47404
#authors Plucienickak, A.
#submission submitted to the EMBL Data Library, August 1994
#description Molecular cloning and sequencing of two complete genomes of
polish isolates of human hepatitis B virus.
#accession S47405
#molecule_type DNA
#residues 1-212 #label PIU
#cross-references EMBL:Z5516; NID:q527435; PID:q527437
#experimental_source subtype ayw4, isolate hb321
REFERENCE S53112
#authors Lal, M.E.; Marzoleni, A.P.; Portu, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53191
#molecule_type DNA
#residues 1-212 #label LA1
#cross-references EMBL:X85283; NID:q736088; PID:q736090
#experimental_source isolate patient Ferrucci1'83
#accession S53309
#molecule_type DNA
#residues 1-212 #label LA2
#cross-references EMBL:X85290; NID:q736114; PID:q736116
#experimental_source isolate patient Castag'83
#accession S53334
#molecule_type DNA
#residues 1-212 #label LA3
#cross-references EMBL:X85300; NID:q736150; PID:q736152
#experimental_source isolate patient Sanna'84
#accession S53364
#molecule_type DNA
#residues 1-212 #label LA4
#cross-references EMBL:X85313; NID:q736194; PID:q736196

```
##experimental_source isolate patient Licheri-1'85
#accession S53249
##molecule_type DNA
##residues 1-212 ##label LA5
##cross-references EMBL:X85306; NID:q736172; PID:q736174
##experimental_source isolate patient Fiore-1'86
#accession S53262
##molecule_type DNA
##residues 1-212 ##label LA6
##cross-references EMBL:X85312; NID:q736191; PID:q736193
##experimental_source isolate patient Licheri'83
#accession S53277
##molecule_type DNA
##residues 30-212 ##label LA7
##cross-references EMBL:X85317; NID:q736211; PID:q736214
##experimental_source patient Giordo-2'86
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be processed

REFERENCE
#authors Galibert, F.; Mandart, E.; Flitoussi, F.; Tlollais, P.;
#journal Nature (1979) 281:646-650
#title Nucleotide sequence of the hepatitis B virus genome (subtype
#cross-references M01D:81012091.
#accession A03711
##molecule_type DNA
##residues 1-212 ##label GAL
##cross-references GB:j02203; NID:q329640; PID:q329642
##experimental_source subtype ayw

GENETICS
#gene C
#superfamily hepatitis B virus core antigen
#alternative_initiators: core protein

FEATURE
KEYWORDS
1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY
#length 212 #molecular_weight 24350 #checksum 782

Query Match 74.2%; Score 1373; DB 1; Length 212;
Best Local Similarity 99.5%; Pred. No. 4,43e-199;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKRGATVELLSFSPDFPSVRDLDTASALYREALESPHCSPHHTALROAIL 88
:|||||
65 SMIDPKRGATVELLSFSPDFPSVRDLDTASALYREALESPHCSPHHTALROAIL 124
:|||||
89 LCGELMTLATWGVNLEDPASRDLVVSYNTNMGKLFROLMFHISCLTFGRETVEIYL 148
|||||
125 LCGELMTLATWGVNLEDPASRDLVVSYNTNMGKLFROLMFHISCLTFGRETVEIYL 184
|||||
149 VSGVWIRTPPAVRPPAPILSTLPETTVVRRGRSPRRRSPRRRSQSR 208
|||||
185 VSGVWIRTPPAVRPPAPILSTLPETTVVRRGRSPRRRSPRRRSQSR 244
|||||
209 ESOC 212
245 ESOC 248

RESULT 2
ENTRY S53207 #type complete
TITLE core antigen - hepatitis B virus (isolate patient
Castaa-2'87)
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate_patient Castaa-2'87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997 0.
```

```
ACCESSIONS S53207
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53207
##molecule_type DNA
##residues 1-183 ##label LA1
##cross-references EMBL:X85289; NID:q736110; PID:q736113
##experimental_source isolate patient Castaa-2'87
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
#superfamily hepatitis B virus core antigen
#alternative_initiators: core protein

FEATURE
KEYWORDS
1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product e antigen #status predicted #label EAG\

SUMMARY
#length 183 #molecular_weight 21102 #checksum 2165

Query Match 74.1%; Score 1373; DB 2; Length 183;
Best Local Similarity 99.5%; Pred. No. 9,53e-199;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKRGATVELLSFSPDFPSVRDLDTASALYREALESPHCSPHHTALROAIL 60
:|||||
66 MDIDPKRGATVELLSFSPDFPSVRDLDTASALYREALESPHCSPHHTALROAIL 125
:|||||
61 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKLFROLMFHISCLTFGRETVEIYL 120
|||||
126 CWGELMTLATWGVNLEDPASRDLVVSYNTNMGKLFROLMFHISCLTFGRETVEIYL 185
|||||
121 SFGVWIRTPPAVRPPAPILSTLPETTVVRRGRSPRRRSPRRRSQSR 180
|||||
186 SFGVWIRTPPAVRPPAPILSTLPETTVVRRGRSPRRRSPRRRSQSR 245
|||||
181 SOC 183
246 SOC 248

RESULT 3
ENTRY S53211 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Castag-1'85 and others)
ALTERNATE_NAMES HBC antigen; Hbe antigen precursor / HBC antigen; pre-C/C
antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate_patient Castag-1'85; isolate patient Ferracuti-1'89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997
ACCESSIONS S53211; S53197
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53211
##molecule_type DNA
##residues 1-212 ##label LA1
##cross-references EMBL:X85291; NID:q736117; PID:q736119
##experimental_source isolate patient Castag-1'85
#accession S53197
##molecule_type DNA
##residues 30-212 ##label LAW
##cross-references EMBL:X85284; NID:q736095; PID:q736098
##experimental_source isolate patient Ferracuti-1'89
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
#superfamily hepatitis B virus core antigen
#alternative_initiators: core protein

FEATURE
KEYWORDS
1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product e antigen #status predicted #label EAG\
```

179-212 #domain carboxyl-terminal propeptide #link EAG #status
SUMMARY #length 212 #molecular-weight 24336 #checksum 746

Query Match 74.1%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 6.50e-199;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 88
QY :|||||
65 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 124
DB 89 LCMGELMTLATVGVNLDPASRDLYSVYNTNMGKLFQOLMFHISCLTFGRVIEYL 148
QY :|||||
125 LCMGELMTLATVGVNLDPASRDLYSVYNTNMGKLFQOLMFHISCLTFGRVIEYL 184
DB 149 VSEGWIRTPPYRPPNAPILSTLPETTVRRRGSPRRRTSPRRRSQSPRRRSOSR 208
QY :|||||
185 VSEGWIRTPPYRPPNAPILSTLPETTVRRRGSPRRRTSPRRRSQSPRRRSOSR 244
DB 209 ESQC 212
QY :|||||
245 ESQC 248

RESULT 4
ENTRY S32204 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C1000)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#varietal subtype ayw, patient C1000
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS S32204
REFERENCE S32202
#authors Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Geroch, W.; Rasenack, J.
#submission submitted to the EMBL Data Library, March 1993
#description identification and sequence analysis of hepatitis B virus DNA in immunological negative infection.
FEATURE S32204
#accession S32204
#molecule_type DNA
##residues 1-212 ##label PRE
##cross-references EMBL:X72702; NID:9288927; PID:9288930
##experimental_source subtype ayw, patient C1000
#note due to a stop codon between the alternative initiators the e antigen precursor cannot be produced

GENETICS C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
FEATURE 1-29
#domain signal sequence #status predicted #label SIG
30-212 #product core antigen #status predicted #label CAG
30-178 #product e antigen #status predicted #label EAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24336 #checksum 770

Query Match 74.1%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 6.50e-199;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 88
QY :|||||
65 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 124
DB 89 LCMGELMTLATVGVNLDPASRDLYSVYNTNMGKLFQOLMFHISCLTFGRVIEYL 148
QY :|||||
125 LCMGELMTLATVGVNLDPASRDLYSVYNTNMGKLFQOLMFHISCLTFGRVIEYL 184

Db 149 VSEGWIRTPPYRPPNAPILSTLPETTVRRRGSPRRRTSPRRRSQSPRRRSOSR 208
QY :|||||
185 VSEGWIRTPPYRPPNAPILSTLPETTVRRRGSPRRRTSPRRRSQSPRRRSOSR 244
DB 209 ESQC 212
QY :|||||
245 ESQC 248

RESULT 5
ENTRY S20750 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient CI)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#varietal subtype ayw, patient CI
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS S20750
REFERENCE S20745
#authors Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Meis, A.; Porru, A.
#submission submitted to the EMBL Data Library, March 1992
#description Sequence analysis of HBV genomes isolated from patients with HBsAg negative chronic liver disease.
FEATURE S20750
#accession S20750
#molecule_type DNA
##residues 1-212 ##label LAI
##cross-references EMBL:X65258; NID:959434; PID:959436
##experimental_source subtype ayw, patient CI

GENETICS C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE 1-29
#domain signal sequence #status predicted #label SIG
30-212 #product core antigen #status predicted #label CAG
30-178 #product e antigen #status predicted #label EAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 147

Query Match 74.1%; Score 1373; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 9.53e-199;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 88
QY :|||||
65 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 124
DB 89 LCMGELMTLATVGVNLDPASRDLYSVYNTNMGKLFQOLMFHISCLTFGRVIEYL 148
QY :|||||
125 LCMGELMTLATVGVNLDPASRDLYSVYNTNMGKLFQOLMFHISCLTFGRVIEYL 184
DB 149 VSEGWIRTPPYRPPNAPILSTLPETTVRRRGSPRRRTSPRRRSQSPRRRSOSR 208
QY :|||||
185 VSEGWIRTPPYRPPNAPILSTLPETTVRRRGSPRRRTSPRRRSQSPRRRSOSR 244
DB 209 ESQC 212
QY :|||||
245 ESQC 248

RESULT 6
ENTRY S53270 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Licheri-2/87)
ALTERNATE_NAMES HBeC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#varietal isolate patient Licheri-2/87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

ACCESSIONS	08-Sep-1997
REFERENCE	S53270
#authors	Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission	Submitted to the EMBL Data Library, March 1995
#accession	S53270
##molecule-type	DNA
##residues	1-183 ##label LAI
##cross-references	EMBL:X85314; NID:g736201; PID:g736204
##experimental_source	isolate patient Licheri-2/87
##note	due to a stop codon between the alternative initiators the e antigen precursor cannot be produced
GENETICS	
CLASSIFICATION	C
KEYWORDS	#superfamily hepatitis B virus core antigen core protein
SUMMARY	length 183 #molecular-weight 21102 #checksum 2199
Query Match	73.9%; Score 1370; DB 2; Length 183;
Best Local Similarity	98.4%; Pred. No. 3.01e-198;
Matches	180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db	1 MDIDPKFGATVELSLPSPDFPPSYRDLDITASALYRDALSPHCSPHNTALROAIL 60 66 MDIDPKFGATVELSLPSPDFPPSYRDLDITASALYRDALSPHCSPHNTALRAL 125
Qy	61 CWMGLMTLATWGVNLDPASRDLVSVYNTNMGKFRQLLMFHSICLTFGRETVIEYL 120 126 CWMGLMTLATWGVNLDPASRDLVSVYNTNMGKFRQLLMFHSICLTFGRETVIEYL 185
Db	121 SFGWIRTPPAYRPNNAILSTLETVYVRRKGTTPRRTPSPRRRSQSPRRRSQSR 180 186 SFGWIRTPPAYRPNNAILSTLETVYVRRKGTTPRRTPSPRRRSQSPRRRSQSR 245
Qy	181 SGC 183 246 SGC 248
RESULT	7
ENTRY	S53216 #type complete
TITLE	e antigen precursor / core antigen - hepatitis B virus (isolate patient Castag/3)
ALTERNATE_NAMES	HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS	core antigen; e antigen
ORGANISM	#formal_name hepatitis B virus; HBV
variety	isolate patient Castag/3
DATE	08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997
ACCESSIONS	S53216
REFERENCE	S53112
#authors	Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission	submitted to the EMBL Data Library, March 1995
#accession	S53216
##molecule-type	DNA
##residues	1-212 ##label LAI
##cross-references	EMBL:X85293; NID:g736124; PID:g736126
##experimental_source	isolate patient Castag/3
GENETICS	
CLASSIFICATION	C
KEYWORDS	#superfamily hepatitis B virus core antigen alternative initiators; core protein
FEATURE	
1-29	#domain signal sequence #status predicted #label SIG\
30-212	#product e antigen #status predicted #label CAG\
179-212	#domain carboxyl-terminal propeptide #link EXG #status predicted #label ECP
SUMMARY	length 212 #molecular-weight 24363 #checksum 752
Query Match	73.9%; Score 1370; DB 2; Length 212;
Best Local Similarity	98.9%; Pred. No. 3.01e-198;
Matches	182; Conservative 1; Indels 0; Gaps 0;

Db	29	GMDIDPYKEFGATVELLSFLPSDFPSVRDLDDNASALYREALESPHCSPHHTALROAI	88
Oy	65	SMMDIDPYKEFGATVELLSFLPSDFPSVRDLDDNASALYREALESPHCSPHHTALROAI	124
Db	89	LCWGEIMTLATWGVNLEDPASRDLYSVYNTNGKLFROLIMFHSICLTFGRETVEYL	148
Oy	125	LCWGEIMTLATWGVNLEDPASRDLYSVYNTNGKLFROLIMFHSICLTFGRETVEYL	184
Db	149	VSFQWINTPPATYRPNAPILSTLPETTVYARRGRSPRRRTPPRRRRSQSPRRRRSQSR	208
Oy	185	VSFQWINTPPATYRPNAPILSTLPETTVYARRGRSPRRRTPPRRRRSQSPRRRRSQSR	244
Db	209	ESQC 212	
Oy	245	ESQC 248	
RESULT	8		
ENTRY		553272	#type complete
TITLE		e antigen precursor / core antigen - hepatitis B virus	
ALTERNATE_NAMES		(isolate patient Licheri-3'90)	
CONTAINS		HBe antigen precursor / Hbc antigen; pre-C/C antigen	
ORGANISM		core antigen; e antigen	
DATE		#formal_name hepatitis B virus, HBV	
		isolate patient Licheri-3'90	
		08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change	
ACCESSIONS		553272	
REFERENCE		553112	
#authors		Lai, M.E.; Marzoli, A.P.; Porru, A.; Balestrieri, A.	
#submission		submitted to the EMBL Data Library, March 1995	
#accession		553272	
#molecule_type		DNA	
#residues		1-212	#label LAI
GENETICS		##cross-references EMBL:X85315; NID:q736205; PID:q736207	
		##experimental_source isolate patient Licheri-3'90	
CLASSIFICATION		C	
KEYWORDS		#superfamily hepatitis B virus core antigen	
FEATURE		alternative initiators; core protein	
1-29			
30-212		#domain signal sequence #status predicted #label SIG\	
30-178		#product e antigen #status predicted #label CAG\	
179-212		#domain carboxyl-terminal propeptide #link EAG #status	
		predicted #label ECP	
SUMMARY		#length 212 #molecular_weight 24366 #checksum 446	
Query Match		73.9%; Score 1370; DB 2; length 212;	
Best Local Similarity		98.9%; Pred. No. 3.01e-198;	
Matches 182; Conservative		1; Mismatches 1; Indels 0; Gaps 0	
Db	29	GMDIDPYKEFGATVELLSFLPSDFPSVRDLDDNASALYREALESPHCSPHHTALROAI	88
Oy	65	SMMDIDPYKEFGATVELLSFLPSDFPSVRDLDDNASALYREALESPHCSPHHTALROAI	124
Db	89	LCWGEIMTLATWGVNLEDPASRDLYSVYNTNGKLFROLIMFHSICLTFGRETVEYL	148
Oy	125	LCWGEIMTLATWGVNLEDPASRDLYSVYNTNGKLFROLIMFHSICLTFGRETVEYL	184
Db	149	VSFQWINTPPATYRPNAPILSTLPETTVYARRGRSPRRRTPPRRRRSQSPRRRRSQSR	208
Oy	185	VSFQWINTPPATYRPNAPILSTLPETTVYARRGRSPRRRTPPRRRRSQSPRRRRSQSR	244
Db	209	ESQC 212	
Oy	245	ESQC 248	
RESULT	9		
ENTRY		553163	#type complete
TITLE		e antigen precursor / core antigen - hepatitis B virus	

ALTERNATE_NAMES (isolate patient Vittorina'92)
CONTAINS HBE antigen precursor / HBC antigen; pre-C/C antigen
ORGANISM core antigen; e antigen
#formal_name hepatitis B virus, HBV
#variety isolate patient Vittorina'92
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53163
REFERENCE S53112
#authors Lal, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53163
#molecule_type DNA
#residues 1-212 #label LAI
##cross-references EMBL:X85256; NID:g736050; PID:g736052
##experimental_source isolate patient Vittorina'92

GENETICS C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG
30-212 #product core antigen #status predicted #label CAG
30-178 #product e antigen #status predicted #label EAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24322 #checksum 842

Query Match 73.8%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 4,42e-198;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHNTALROAI 88
:|||||
65 SMDIDPKFEGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHNTALROAI 124
:|||||

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNGLKFKRLMFIHISCLTGFRETVEYL 148
:|||||
125 LCMGELMTLATWGVNLEDPASRDVSVYNTNGLKFKRLMFIHISCLTGFRETVEYL 184
:|||||

Db 149 VSFQWIRTPAPYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSOSPRRRRSOSR 208
:|||||
185 VSFQWIRTPAPYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSOSPRRRRSOSR 244
:|||||

Qy 209 ESOC 212
:|||||
Qy 245 ESOC 248

RESULT 10
ENTRY S20746 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C)
ALTERNATE_NAMES HBE antigen precursor / HBC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety subtype ayw, patient C
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997

ACCESSIONS S20746
REFERENCE S20745
#authors Lal, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.;
Porru, A.
#submission submitted to the EMBL Data Library, March 1992
#description Sequence analysis of HBV genomes isolated from patients with
HBsAg negative chronic liver disease.
#accession S20746
#molecule_type DNA
#residues 1-212 #label LAI
##cross-references EMBL:X65257; NID:g959429; PID:g959431
##experimental_source subtype ayw, patient C

GENETICS C
#gene

CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG
30-212 #product core antigen #status predicted #label CAG
30-178 #product e antigen #status predicted #label EAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 506

Query Match 73.8%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 4,42e-198;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHNTALROAI 88
:|||||
65 SMDIDPKFEGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHNTALROAI 124
:|||||

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNGLKFKRLMFIHISCLTGFRETVEYL 148
:|||||
125 LCMGELMTLATWGVNLEDPASRDVSVYNTNGLKFKRLMFIHISCLTGFRETVEYL 184
:|||||

Db 149 VSFQWIRTPAPYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSOSPRRRRSOSR 208
:|||||
185 VSFQWIRTPAPYRPPNAPILSTLPETTVVRRGRSPRRRPSRRRSOSPRRRRSOSR 244
:|||||

Db 209 ESOC 212
:|||||
Qy 245 ESOC 248

RESULT 11
ENTRY S53225 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Chighine-2'86)
ALTERNATE_NAMES HBE antigen precursor / HBC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Chighine-2'86
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53225
REFERENCE S53112
#authors Lal, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53225
#molecule_type DNA
#residues 1-212 #label LAI
##cross-references EMBL:X85296; NID:g736137; PID:g736139
##experimental_source isolate patient Chighine-2'86

GENETICS C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG
30-212 #product core antigen #status predicted #label CAG
30-178 #product e antigen #status predicted #label EAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24308 #checksum 655

Query Match 73.8%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 4,42e-198;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHNTALROAI 88
:|||||
65 SMDIDPKFEGATVELLSFSPDFPSVRDLDTASALYREALSPHCSPHNTALROAI 124
:|||||

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNGLKFKRLMFIHISCLTGFRETVEYL 148
:|||||
125 LCMGELMTLATWGVNLEDPASRDVSVYNTNGLKFKRLMFIHISCLTGFRETVEYL 184
:|||||

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Db      149 VSEGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPSPRRRSQSRRRRRSQSR 208
      185 VSEGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPSPRRRSQSRRRRRSQSR 244
QY      209 ESOC 212
      245 ESOC 248

RESULT  12
ENTRY   S53198
TITLE   #type complete
        e antigen precursor / core antigen - hepatitis B virus
        (isolate patient Ferracuti-2'90)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORANISM #formal_name hepatitis B virus, HBV
        isolate patient Ferracuti-2'90
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
        08-Sep-1997

ACCESSIONS S53198
REFERENCE S53112
AUTHORS Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
SUBMISSION submitted to the EMBL Data Library, March 1995
#accession S53198
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85285; NID:g736099; PID:g736100
#experimental_source isolate patient Ferracuti-2'90

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
        predicted #label ECP
SUMMARY #length 212 #molecular-weight 24292 #checksum 593

Query Match 73.8%; Score 1368; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 6,48e-198;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      29 GMDIDPKKEGATVELLSFLPSAFPPSVRDLDITASALYREALSPHCSPHHTALRQAI 88
      65 SMDIDPKKEGATVELLSFLPSDFPSVDLDITASALYREALSPHCSPHHTALRQAI 124
QY      89 LCMGDLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLHFHISCLTFGRRETVIEYL 148
      125 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLHFHISCLTFGRRETVIEYL 184
Db      149 VSEGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPSPRRRSQSRRRRRSQSR 208
      185 VSEGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPSPRRRSQSRRRRRSQSR 244
QY      209 ESOC 212
      245 ESOC 248

RESULT  13
ENTRY   S53223
TITLE   #type complete
        e antigen precursor / core antigen - hepatitis B virus
        (isolate patient Chighine-1'85)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORANISM #formal_name hepatitis B virus, HBV
        isolate patient Chighine-1'85
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
        08-Sep-1997

ACCESSIONS S53223

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REFERENCE S53112
AUTHORS Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
SUBMISSION submitted to the EMBL Data Library, March 1995
#accession S53223
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85295; NID:g736134; PID:g736136
#experimental_source isolate patient Chighine-1'85

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
        predicted #label ECP
SUMMARY #length 212 #molecular-weight 24364 #checksum 1123

Query Match 73.7%; Score 1366; DB 2; Length 212;
Best Local Similarity 97.8%; Pred. No. 1.39e-197;
Matches 180; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db      29 GMDIDPKKEGATVELLSFLPSDFPSVDLDITASALYREALSPHCSPHHTALRQAI 88
      65 SMDIDPKKEGATVELLSFLPSDFPSVDLDITASALYREALSPHCSPHHTALRQAI 124
QY      89 LCMGDLMTLATWGVNLEDPISRDLYSVYNTNMGKLFROLMLHFHISCLTFGRRETVIEYL 148
      125 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMLHFHISCLTFGRRETVIEYL 184
Db      149 VSEGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPSPRRRSQSRRRRRSQSR 208
      185 VSEGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPSPRRRSQSRRRRRSQSR 244
QY      209 ESOC 212
      245 ESOC 248

RESULT  14
ENTRY   S53274
TITLE   #type complete
        e antigen precursor / core antigen - hepatitis B virus
        (isolate patient Giordo'84)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORANISM #formal_name hepatitis B virus, HBV
        isolate patient Giordo'84
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
        08-Sep-1997

ACCESSIONS S53274
REFERENCE S53112
AUTHORS Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
SUBMISSION submitted to the EMBL Data Library, March 1995
#accession S53274
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85316; NID:g736208; PID:g736210
#experimental_source isolate patient Giordo'84

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
        predicted #label ECP
SUMMARY #length 212 #molecular-weight 24376 #checksum 390

Query Match 73.7%; Score 1366; DB 2; Length 212;

```

Best Local Similarity 98.9%; Pred. No. 1.39e-197;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPFSVRLDLDTSALYREALSPHCHSPHHTALRQAI 88
:|||||
OY 65 SMDIDPYKEFGATVELLSFLPSDFPFSVRLDLDTSALYREALSPHCHSPHHTALRQAI 124
:|||||

Db 89 LCMGELMTLATWGVNLEDPRASRDLYSVYNTNMGKFRQLMFHISCLTFGRETIVIEYL 148
:|||||
OY 125 LCMGELMTLATWGVNLEDPRASRDLYSVYNTNMGKFRQLMFHISCLTFGRETIVIEYL 184
:|||||

Db 149 VSFQWIRTPPAYRPPNAPILTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
:|||||
OY 185 VSFQWIRTPPAYRPPNAPILTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 244
:|||||

Db 209 ESQC 212
:|||||
OY 245 ESQC 248
:|||||

RESULT 15
ENTRY S53169 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Muresu'89)
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Muresu'89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53169
REFERENCE S53112
#author Lal, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53169
##molecule_type DNA
##residues 1-183 ##label LAI
##cross-references EMBL:X85275; NID:g736057; PID:g736060
##experimental_source isolate patient Muresu'89
##note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
SUMMARY #length 183 #molecular-weight 21088 #checksum 1849

Query Match 73.6%; Score 1364; DB 2; Length 183;
Best Local Similarity 98.4%; Pred. No. 3.00e-197;
Matches 180; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDIDPYKEFGATVELLSFLPSDFPFSVRLDLDTSALYREALSPHCHSPHHTALRQAI 60
:|||||
OY 66 MDIDPYKEFGATVELLSFLPSDFPFSVRLDLDTSALYREALSPHCHSPHHTALRQAI 125
:|||||

Db 61 CMGELMTLATWGVNLEDPRASRDLYSVYNTNMGKFRQLMFHISCLTFGRETIVIEYL 120
:|||||
OY 126 CMGELMTLATWGVNLEDPRASRDLYSVYNTNMGKFRQLMFHISCLTFGRETIVIEYL 185
:|||||

Db 121 SFGWIRTPPAYRPPNAPILTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
:|||||
OY 186 SFGWIRTPPAYRPPNAPILTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 245
:|||||

Db 181 SQC 183
:|||||
OY 246 SQC 248
:|||||

Search completed: Thu Dec 16 13:01:29 1999
Job time : 62 secs.

 WISE (TM)

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Dec 16 13:01:46 1999; MasPar time 8.80 seconds
 Tabular output not generated. 796.747 Million cell updates/sec

Title: >US3835-1-38183
 Description: (1-248) from us3835-1-38183.pep
 Perfect Score: 1854
 Sequence: 1 MDIDPYKEFGATVELLSFLP.....RRRRSQSPRRRRSQSRESQC 248

Scoring table: PAM 150
 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 48.750; Variance 106.745; scale 0.457

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1374	74.1	183	1	CORA_HPBVA CORE ANTIGEN.	6.54e-229
2	1358	73.2	211	1	CORA_HPBVA CORE ANTIGEN.	7.60e-226
3	1349	72.8	183	1	CORA_HPBVA CORE ANTIGEN.	4.02e-224
4	1346	72.1	183	1	CORA_HPBVA CORE ANTIGEN.	1.24e-221
5	1334	72.0	183	1	CORA_HPBVA CORE ANTIGEN.	3.00e-221
6	1322	71.3	183	1	CORA_HPBVA CORE ANTIGEN.	5.93e-219
7	1321	71.3	185	1	CORA_HPBVA CORE ANTIGEN.	9.22e-219
8	1314	70.9	195	1	CORA_HPBVA CORE ANTIGEN.	2.01e-217
9	1313	70.8	212	1	CORA_HPBVA CORE ANTIGEN.	3.13e-217
10	1308	70.6	183	1	CORA_HPBVA CORE ANTIGEN.	2.83e-216
11	1305	70.4	185	1	CORA_HPBVA CORE ANTIGEN.	1.06e-215
12	1304	70.3	214	1	CORA_HPBVA CORE ANTIGEN.	1.65e-215
13	938	50.6	217	1	CORA_HPBVA CORE ANTIGEN.	5.93e-146
14	934	50.4	217	1	CORA_HPBVA CORE ANTIGEN.	3.37e-145
15	933	50.3	187	1	CORA_HPBVA CORE ANTIGEN.	5.20e-145
16	234	12.6	289	1	CERP_MESAV CHOLESTERYL ESTER TRAN	4.53e-19
17	234	12.6	493	1	CERP_MACRA CHOLESTERYL ESTER TRAN	4.53e-19
18	234	12.6	493	1	CERP_HUMAN CHOLESTERYL ESTER TRAN	4.53e-19
19	200	10.8	305	1	CORA_HPBVA CORE ANTIGEN.	9.28e-14
20	200	10.8	305	1	CORA_HPBVA CORE ANTIGEN.	9.28e-14
21	200	10.8	305	1	CORA_HPBVA CORE ANTIGEN.	9.28e-14
22	200	10.8	305	1	CORA_HPBVA CORE ANTIGEN.	9.28e-14
23	200	10.8	305	1	CORA_HPBVA CORE ANTIGEN.	9.28e-14

ID	Accession	Standard	Prot	Length	Score	Description
24	200	10.8	497	1	CERP_RABIT	CHOLESTERYL ESTER TRAN
25	158	8.5	196	1	SER2_CAEL	POTATIVE SPLICING FACT
26	148	8.0	208	1	YSX2_CAEL	HYPOTHETICAL 24.0 KD P
27	136	7.3	78	1	PR1_SEPOF	SPEMATID-SPECIFIC PRO
28	131	7.1	61	1	HSP1_MACRU	SPEM PROTAMINE P1
29	130	7.0	77	1	PR2_SEPOF	SPEMATID-SPECIFIC PRO
30	126	6.8	498	1	VE2_HPV08	REGULATORY PROTEIN E2
31	126	6.8	1523	1	SON_HUMAN	SON PROTEIN (SON3)
32	124	6.7	57	1	HSP1_DIDNA	SPEM PROTAMINE P1
33	125	6.7	60	1	HSP1_MACGI	SPEM PROTAMINE P1
34	125	6.7	61	1	HSP1_MACRG	SPEM PROTAMINE P1
35	122	6.6	91	1	PH1_MATED	SPEM-SPECIFIC PROTEIN
36	122	6.6	132	1	PR1_ANTGR	PROTAMINE
37	121	6.5	61	1	HSP1_CHICK	SPEM HISTONE (PROTAMI
38	121	6.5	739	1	DL13_CAEL	PEPTIDYLPROLYL ISOMERA
39	121	6.5	843	1	CYPL1_BROWA	SPEM PROTAMINE P1 (CY
40	119	6.4	50	1	HSP1_RAT	SPEM PROTAMINE P1 (CY
41	119	6.4	50	1	HSP1_MOUSE	SPEM PROTAMINE P1 (CY
42	118	6.4	238	1	SER7_HUMAN	SPLICING FACTOR, ARGIN
43	118	6.4	576	1	CAT1_RHOCA	PEROXIDASE / CATALASE
44	115	6.2	102	1	HSP2_MACRU	SPEM HISTONE P2 PRECU
45	115	6.2	104	1	HSP2_CALJA	SPEM HISTONE P2 PRECU

ALIGNMENTS

RESULT 1
 ID CORA_HPBVA STANDARD: PR1: 183 AA.
 AC P03146: 1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN C.
 OS HEPATITIS B VIRUS (SUBTYPE AYW).
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA GALIBERT F., MANDART E., FITOUSSI F., TIOLLAIS P., CHARNAY P.;
 RT "Nucleotide sequence of the hepatitis B virus genome (subtype ayw)"
 RL NATURE 281:646-650(1979).
 RP SEQUENCE FROM N.A. (CLONE PHB320).
 RX MEDLINE: 85204397.
 RA BICHKO V., PUSHKO P., DRELLINA D., PUMPEIN P., GREN E.;
 RT "Subtype ayw variant of hepatitis B virus. DNA primary structure
 analysis.";
 RL FEBS LETT. 185:208-212(1985).
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 CC EMBL: V01460; G62278; ALT.INT.
 DR EMBL: X02496; -; NOT_ANNOTATED_CDS.
 DR PIR: A03711; NRYLAH.
 DR PIR: A03712; NRYLAH.
 DR PIR: P00906; Hepatitis_core.1.
 CC CORE PROTEIN: REPEAT.
 FT REPEAT 162 169
 FT REPEAT 170 177
 FT CONFLICT 33 33 T -> N (IN REF. 2).
 FT CONFLICT 80 80 A -> I (IN REF. 2).
 SQ SEQUENCE 183 AA; 2116 MW; 2AE7A17A CRC32;
 Query Match 74.1%; Score 1374; DB 1; Length 183;
 Best Local Similarity 100.0%; Pred. No. 6.54e-229;


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J. GEN. VIROL. 69:2575-2583(1988).
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CC -----
CC EMBL; D00330; ; NOT_ANNOTATED_CDS.
DR PIR; B28925; NKVLJ2.
DR PFAM; PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 115BD9E3 CRC32;
-----
Query Match 72.1%; Score 1336; DB 1; Length 183;
Best Local Similarity 96.2%; Pred No. 1 24e-221;
Matches 176; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
-----
Db 1 MDIDPKKFGASVELLSFLPSDFPSVVDLDTASALYREALSEPHKSPHHTALROAIL 60
Qy 66 MDIDPKKFGATVELLSFLPSDFPSVVDLDTASALYREALSEPHKSPHHTALROAIL 125
Db 61 CWGELMNLATWGSLEDPASRELYSVYVNVNMGKLRQLRMFHSICLTFGRETYLEIY 120
Qy 126 CWGELMTLATWGVLEDPASRDLYSVYVNTMGKFRQLRMFHSICLTFGRETYLEIY 185
Db 121 SFGVWIRTPPAVPPNAPILSTLPETVYVRRGRSPRRRTSPRRRSQSPRRRSQSPRE 180
Qy 186 SFGVWIRTPPAVPPNAPILSTLPETVYVRRGRSPRRRTSPRRRSQSPRRRSQSPRE 245
Db 181 SQC 183
Qy 246 SQC 248
-----
RESULT 5 STANDARD: PRT: 183 AA.
ID 1D CORA_HPBV4
AC P03150; P03151;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADR), HEPATITIS B VIRUS (SUBTYPE ADR4),
OS AND HEPATITIS B VIRUS (SUBTYPE ADM / STAIN INDONESIA/PIDM420).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
CC [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-ADR:
RX MEDLINE: 83168919.
RX ONO Y., OSAIDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adm."
RL NUCLEIC ACIDS RES. 11:1747-1757(1983).
RN [2]
RN RP SEQUENCE FROM N.A.
RC STRAIN-ADR4;
RX MEDLINE: 83246570.
RX FUJIYAMA A., MIYANOHARA A., NOZAKI C., YONEYAMA T., OTOMO N.,
RA MATSUBARA K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr."
RL NUCLEIC ACIDS RES. 11:4601-4610(1983).
RN [3]
RN RP SEQUENCE FROM N.A.
RC STRAIN-ADM;
RX MEDLINE: 89010694.
RX OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEMIWUNJO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;

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RT "Typing hepatitis B virus by homology in nucleotide sequence:
RL Comparison of surface antigen subtypes.",
J. GEN. VIROL. 69:2575-2583(1988).
-----
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-----
DR EMBL: V00867; -. NOT_ANNOTATED_CDS.
DR EMBL: X01587; G59407; -.
DR EMBL: D00031; -. NOT_ANNOTATED_CDS.
DR PIR: A93480; NKVL45.
DR PIR: B93460; NKVL44.
DR PIR: C28925; NKVLJ3.
DR PIR: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21095 MW; D2E185B9 CRC32;
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Query Match 72.0%; Score 1334; DB 1; Length 183;
Best Local Similarity 95.6%; Pred. No. 3,00e-22;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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Db 1 MDIDYKFGASVELLSFLPSDFPSPIRDLDLTASALYREALSEPHCSPHNTALROAIL 60
QY 66 MDIDYKFGAGAVELLSFLPSDFPSPVSDLDLTALALREALSEPHCSPHNTALROAIL 125
-----
Db 61 CGEELMNLATWGSWLEDPASRELIVSYVNNMGKIQQLMFHISCLTFGEYLEYLY 120
QY 126 CGEELMNLATWGSWLEDPASRDLYVSYVNTMGKIFQLLMFHISCLTFGEYLEYLY 185
-----
Db 121 SFGVIRTPPAAPRNAPNALISTLEPTTVVRRGRSPRRTPSPRRRSOSPPRRRSOSNE 180
QY 186 SFGVIRTPPAAPRNAPNALISTLEPTTVVRRGRSPRRTPSPRRRSOSPPRRRSOSNE 245
-----
Db 181 SOC 183
QY 246 SOC 248
-----
RESULT 6
ID ID CORA_HPBVJ STANDARD; PRT; 183 AA.
AC P17391;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
OS HEPATITIS B VIRUS (SUBTYPE ADM / STRAIN JAPAN/PJDM2233).
OC VIRUSES; RETROID VIRUSES; HERPDNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWICIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. GEN. VIROL. 69:2575-2583(1988).
-----
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-----
DR EMBL: D00329; -. NOT_ANNOTATED_CDS.
DR PIR: A28925; NKVLJ1.

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DR PFAM: PF00906; Hepatitis_core; 1.
 KW CORE PROTEIN; REPEAT.
 FT REPEAT 162 169
 FT REPEAT 170 177
 FT REPEAT 183 185
 SQ SEQUENCE 183 AA; 21224 MW; F6B348B6 CRC32;

Query Match
 Best Local Similarity 96.2%; Pred. No. 5.93e-219;
 Matches 176; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 MDIDPYKEGATVLLSFLPSDFPSVRLDLDITASALYREALKSPHCSPHHTLRQAII 60
 |||||||
 QY 66 MDIDPYKEGATVLLSFLPSDFPSVRLDLDITASALYREALKSPHCSPHHTLRQAII 125
 |||||||
 Db 61 CWGELMTLATVGNLDPASRDLYVNVNTNMGKIRQLMWHFISCLTFRGVLEYLY 120
 |||||||
 QY 126 CWGELMTLATVGNLDPASRDLYVNVNTNMGKIRQLMWHFISCLTFRGVLEYLY 185
 |||||||
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSRE 180
 |||||||
 QY 186 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSRE 245
 |||||||
 Db 181 SOC 183
 |||
 QY 246 SOC 248

RESULT 7
 ID CORA_HPBVT STANDARD; PRT; 185 AA.
 AC P03119;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN C.
 OS HEPATITIS B VIRUS (SUBTYPE ADW).
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 83168919.
 RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 RT DNA; subtype adw and adw.";
 RL NUCLEIC ACIDS RES. 11:1747-1757(1983).
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 CC
 CC EMBL: V00866; NOT_ANNOTATED_CDS.
 DR PIR: C93460; NKLVL6.
 DR PFAM: PF00906; Hepatitis_core; 1.
 KM CORE PROTEIN; REPEAT.
 FT REPEAT 164 171
 FT REPEAT 172 179
 FT REPEAT 185 185
 SQ SEQUENCE 185 AA; 21394 MW; 791E0381 CRC32;

Query Match
 Best Local Similarity 96.2%; Pred. No. 9.22e-219;
 Matches 178; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Db 1 MDIDPYKEGATVLLSFLPSDFPSVRLDLDITASALYREALKSPHCSPHHTLRQAII 60
 |||||||
 QY 66 MDIDPYKEGATVLLSFLPSDFPSVRLDLDITASALYREALKSPHCSPHHTLRQAII 125
 |||||||
 Db 61 CWGELMTLATVGNLDPASRDLYVNVNTNMGKIRQLMWHFISCLTFRGVLEYLY 120
 |||||||
 QY 126 CWGELMTLATVGNLDPASRDLYVNVNTNMGKIRQLMWHFISCLTFRGVLEYLY 185
 |||||||

Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQS 180
 |||||||
 QY 186 SFGWIRTPPAYRPPNAPILSTLPETTVVRR--GSPRRRTSPRRRSQSPRRRSQS 243
 |||||||
 Db 181 RESOC 185
 |||||
 QY 244 RESOC 248

RESULT 8
 ID CORA_HPBVT STANDARD; PRT; 195 AA.
 AC P29178;
 DT 01-DEC-1992 (REL. 24, CREATED)
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN C.
 OS HEPATITIS B VIRUS (SUBTYPE ADW2 VARIANT SF).
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90169850.
 RA BHAT R.A., ULRICH P.P., VYAS G.N.;
 RT "Molecular characterization of a new variant of hepatitis B virus in
 RT a persistently infected homosexual man.";
 RL HEPATOLOGY 11:271-276(1990).
 DR PIR: A37182; NKLVL3.
 DR PFAM: PF00906; Hepatitis_core; 1.
 KM CORE PROTEIN; REPEAT.
 FT REPEAT 174 181
 FT REPEAT 182 189
 FT REPEAT 195 195
 SQ SEQUENCE 195 AA; 22461 MW; AF3DB5F3 CRC32;

Query Match
 Best Local Similarity 93.5%; Pred. No. 2.01e-217;
 Matches 173; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 11 FGDLIDPYKEGATVLLSFLPSDFPSVRLDLDITASALYREALKSPHCSPHHTLRQA 70
 |||||||
 QY 64 LSMDIDPYKEGATVLLSFLPSDFPSVRLDLDITASALYREALKSPHCSPHHTLRQA 123
 |||||||
 Db 71 ILGWELMTLATVGNLDPASRDLYVNVNTNMGKIRQLMWHFISCLTFRGVLEYLY 130
 |||||||
 QY 124 ILGWELMTLATVGNLDPASRDLYVNVNTNMGKIRQLMWHFISCLTFRGVLEYLY 183
 |||||||
 Db 131 LVSGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQS 190
 |||||||
 QY 184 LVSGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQS 243
 |||||||
 Db 191 RESOC 195
 |||||
 QY 244 RESOC 248

RESULT 9
 ID CORA_HPBVT STANDARD; PRT; 212 AA.
 AC Q05495;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN C.
 OS HEPATITIS B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE W4B).
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93346970.
 RA NAUMANN H., SCHAEFER S., YOSHIDA C.F.T., GASPAR A.M.C., REPP R.,
 RA GERLICH W.H.;
 RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
 RT that expresses HBV surface antigen subtype adw4.";
 RL J. GEN. VIROL. 74:1627-1632(1993).
 CC

Query Match	Best Local Similarity	Matches	70.6%	Score 1308;	DB 1;	Length 183;
Matches	173;	Conservative	6;	Mismatches	4;	Indels
Db	1	MDIDPYKEFGATVLLSFLPSDFPSVRDLDDTASALYREALSEPHCSPHHTALROAIL	60			
Qy	66	MDIDPYKEFGATVLLSFLPSDFPSVRDLDDTASALYREALSEPHCSPHHTALROAIL	125			
Db	61	CWGLMELTATVAVGNLDDPASRDVAVYVNTNMGKIRQLIMFHSICLTGRETIVLEYLV	120			
Qy	126	CWGLMELTATVAVGNLDDPASRDVAVYVNTNMGKIRQLIMFHSICLTGRETIVLEYLV	185			
Db	121	SFGWIRTPPAIRPPNAPILSTLDETIVVRRGRSPRRRTSPRRRSOSPPRRRSOSPA	180			
Qy	186	SFGWIRTPPAIRPPNAPILSTLDETIVVRRGRSPRRRTSPRRRSOSPPRRRSOSRE	245			
Db	181	SQC 183				
Qy	246	SQC 248				
RESULT	11	STANDARD;	PRT;	185	AA.	
ID	CORA_HPBV2					
AC	P03148;					
DT	21-JUL-1986 (REL. 01, CREATED)					
DT	01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)					
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)					
DE	CORE ANTIGEN.					
GN	C.					
OS	HEPATITIS B VIRUS (SUBTYPE ADM2).					
OC	VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	VALENUELA P., QUIROGA M., ZALDIVAR J., GRAY P., RUTTER W.J.;					
RL	(IN) FIELD B.N., JAEINISCH R., FOX C.F. (EDS.);					
RL	ANIMAL VIRUS GENETICS, PP.57-70, ACADEMIC PRESS, NEW YORK (1980).					
DR	PIR: A94409; NIKYLA3.					
PFAM:	PF00906; Hepatitis_core: 1.					
KM	CORE PROTEIN; REPEAT.					
FT	REPEAT 164 171					
FT	REPEAT 172 179					
SEQUENCE	185 AA; 21304 MW; E2EA3360 CRC32;					
Query Match	Best Local Similarity	Matches	70.4%;	Score 1305;	DB 1;	Length 185;
Db	1	MDIDPYKEFGATVLLSFLPSDFPSVRDLDDTASALYREALSEPHCSPHHTALROAIL	60			
Qy	66	MDIDPYKEFGATVLLSFLPSDFPSVRDLDDTASALYREALSEPHCSPHHTALROAIL	125			
Db	61	CWGLMELTATVAVGNLDDPASRDVAVYVNTNMGKIRQLIMFHSICLTGRETIVLEYLV	120			
Qy	126	CWGLMELTATVAVGNLDDPASRDVAVYVNTNMGKIRQLIMFHSICLTGRETIVLEYLV	185			
Db	121	SFGWIRTPPAIRPPNAPILSTLDETIVVRRGRSPRRRTSPRRRSOSPPRRRSOS	180			
Qy	186	SFGWIRTPPAIRPPNAPILSTLDETIVVRRGRSPRRRTSPRRRSOSPPRRRSOS	243			
Db	181	RESQC 185				
Qy	244	RESQC 248				
RESULT	12	STANDARD;	PRT;	214	AA.	
ID	CORA_HPBV9					
AC	P17099;					
DT	01-AUG-1990 (REL. 15, CREATED)					
DT	01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)					
DT	01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)					
DE	CORE ANTIGEN.					
GN	C.					

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OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN 991).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA KOEHEL H.G., SCHUELER A., LOTTMANN S., THOMSEN R.;
RE SUBMITTED (FEB-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
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CC -----
CC EMBL; X51970; G60433; -.
DR PIR; S10381; NKVLKS.
DR PFAM; PF00906; Hepatitis_core; 1.
KM CORE PROTEIN; REPEAT
FT REPEAT 193 200
FT REPEAT 201
SQ SEQUENCE 214 AA; 24722 MW; 786CD048 CRC32;

Query Match
Best Local Similarity 70.3%; Score 1304; DB 1; Length 214;
Matches 177; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Db 29 GMDIDYKKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALROAI 88
QY 65 SMDIDYKKEFGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALROAI 124
Db 89 LCMGELMTLATVGNVLEDPASRDVAVNTVMGKTRQQLMFRISYTLFGREIVLEYL 148
QY 125 LCMGELMTLATVGNVLEDPASRDVAVNTVMGKTRQQLMFRISYTLFGREIVLEYL 184
Db 149 VSGFWIRTPAPRPAPNPADILSTLPETVYRRRDRGRSPRRRPSRRRSQSPRRRSQ 208
QY 185 VSGFWIRTPAPRPAPNPADILSTLPETVYRRR--GRSPRRRTPSPRRRSQSPRRRSQ 242
Db 209 SRESOC 214
QY 243 SRESOC 248

RESULT 13
ID CORA_MHV1 STANDARD; PRT: 188 AA.
AC P03152;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 1 (MHV 1),
OS WOODCHUCK HEPATITIS VIRUS 7 (MHV 7),
OS WOODCHUCK HEPATITIS VIRUS 59 (MHV 59), AND
OS WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE) (MHV 8).
OC WOODCHUCK HEPATITIS VIRUS; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA GALTHER F., CHEN T.N., MANDART E.;
RE "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT comparison with the hepatitis B virus sequence.";
RL J. VIROL. 41:51-65(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=WOODCHUCK HEPATITIS VIRUS 7, AND WOODCHUCK HEPATITIS VIRUS 59;
RX MEDLINE; 88101359.
RA COHEN J.I., MILLER R.H., ROSENBLUM B., DENNISTON K., GERIN J.L.,
RA PURCELL R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RT shows conservation of the genome.";
```

```
RL VIROLOGY 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE);
RX MEDLINE; 89144524.
RA GIRONES R., COTE P.J., HORNBUCKLE W.E., TENNANT B.C., GERIN J.L.,
RA PURCELL R.H., MILLER R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RT hepatitis virus that is infectious in the natural host.";
RL PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
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CC -----
CC EMBL; J02442; G336129; -.
DR EMBL; M18752; G336140; -.
DR EMBL; M19183; G336145; -.
DR EMBL; J04514; G336149; -.
DR PIR; A03713; NKVLC.
DR PIR; G32387; NKVLC.
DR PIR; G32387; NKVLC4.
DR PIR; G32397; NKVLC3.
DR PFAM; PF00906; Hepatitis_core; 1.
KM CORE PROTEIN; REPEAT
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; A667DB27 CRC32;

Query Match
Best Local Similarity 50.6%; Score 938; DB 1; Length 188;
Matches 126; Conservative 25; Mismatches 32; Indels 5; Gaps 1;

Db 1 MDIDYKKEGSSYQLNPLDLPDPDLNVLDTATAYEEELTGREHSCPHHTALROAI 60
QY 66 MDIDYKKEGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALROAI 125
Db 61 CWDDELKLIAMMSNITSEQVRIIVNVHNDTWGKLVKROSLSMELSCILFGQHTQGEELY 120
QY 126 CWDGELMTLATVGNVLEDPASRDVAVNTVMGKTRQQLMFRISYTLFGREIVLEYL 185
Db 121 SFGWIRTPAPRPAPNPADILSTLPETVYRRRGAGARSPPRRRPSRRRSQSPRRRR 180
QY 186 SFGWIRTPAPRPAPNPADILSTLPETVYRRRG-----RSPRRRTPSPRRRSQSPRRRR 240
Db 181 SOSPSANC 188
QY 241 SOSRESOC 248

RESULT 14
ID CORA_HPBGS STANDARD; PRT: 217 AA.
AC P03153;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS GROUND SQUIRREL HEPATITIS VIRUS (GSHV).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA SEEBER C., GANEM D., VARMS H.E.;
RT "Nucleotide sequence of an infectious molecularly cloned genome of
RT ground squirrel hepatitis virus.";
RL J. VIROL. 51:367-375(1984).
CC -----
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CC -----
DR EMBL; K02715; G325401; -
DR PIR; A03715; NKVL5.
DR PFAM; PF00906; Hepatitis_core.1.
DR CORE_PROTEIN; REPEAT.
FT REPEAT 196 203
FT REPEAT 204 211
SQ SEQUENCE 217 AA; 25189 MW; B70A00B1 CRC32;

Query Match 50.4%; Score 934; DB 1; Length 217;
Best Local Similarity 68.1%; Pred. No. 3,37e-145;
Matches 128; Conservative 22; Mismatches 32; Indels 6; Gaps 2;

Db 31 MDIDPYKEFGSSYOLLNPLPLDFPPDLNALVDYATALYEELTGREHCSPHHTAIRQALV 90
QY 66 MDIDPYKEFGATVLLSFLPSDFPSVRLDLDTSALYREALSEPHCSPHHTAIRQAL 125

Db 91 CWELTKLIAMSSNITSEQVRIIVNHNVTWGLKVRQSLMFLHLSCLTFGQHTVQEFV 149
QY 126 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLMFHSCLTFGRETIVLEYLV 185

Db 150 SFGVWIRTPAPYRPPNAPILSTLPEHTVIRRGSGARASPRRRTPSPRRRSOSPRRRR 209
QY 186 SFGVWIRTPAPYRPPNAPILSTLPEHTVIRRGSGARASPRRRTPSPRRRSOSPRRRR 240

Db 210 QSPSANC 217
QY 241 QSPRESQC 248

RESULT 15
ID CORA_MHV8 STANDARD; PRT; 187 AA.
AC P06433;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 8 (MHV 8).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86062931.
RA KODAMA K., OGASAWARA N., YOSHIKAWA H., MURAKAMI S.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RL J. VIROL. 56:978-986(1985).
CC -----
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CC -----
DR EMBL; M11082; G336135; -
DR PIR; A03714; NKVL2.
DR PFAM; PF00906; Hepatitis_core.1.
DR CORE_PROTEIN; REPEAT.
FT REPEAT 166 173
FT REPEAT 174 181
SQ SEQUENCE 187 AA; 21579 MW; A1C354F3 CRC32;

Query Match 50.3%; Score 933; DB 1; Length 187;
Best Local Similarity 66.3%; Pred. No. 5.20e-145;
Matches 124; Conservative 26; Mismatches 33; Indels 4; Gaps 2;

Db 1 MDIDPYKEFGSSYOLLNPLPLDFPPDLNALVDYATALYEELTGREHCSPHHTAIRQALV 60
QY 66 MDIDPYKEFGATVLLSFLPSDFPSVRLDLDTSALYREALSEPHCSPHHTAIRQAL 125

Db 61 CWELTKLIAMSSNITSEQVRIIVNHNVTWGLKVRQSLMFLHLSCLTFGQHTVQEFV 120
QY 126 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLLMFHSCLTFGRETIVLEYLV 185

Db 121 SFGVWIRTPAPYRPPNAPILSTLPEHTVIRRGSGARASPRRRTPSPRRRSOSPRRRR 180
QY 186 SFGVWIRTPAPYRPPNAPILSTLPEHTVIRRGSGARASPRRRTPSPRRRSOSPRRRR 241

Db 181 QSPSANC 187
QY 242 QSPRESQC 248

Search completed: Thu Dec 16 13:02:25 1999
Job time : 39 secs.

 [M] [O] [D] [E] [R] [N] [E] [H]
 (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Dec 16 13:02:42 1999; MasPar time 18.20 Seconds
 Tabular output not generated. 743.783 Million cell updates/sec

Title: >US3835-1-38183
 Description: (1-248) from US3835-1-38183.pep
 Perfect Score: 1854
 Sequence: 1 MDIDPKKEGATVELLSFLP.....RRRSOSPRRRRSQSRESQC 248

Scoring table: PAM 150
 Gap 11

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: spltemb19
 1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
 5:sp.invertebrate 6:sp.mammal 7:sp_mhc 8:sp.organelle
 9:sp.phage 10:sp.plant 11:sp_rodent 12:sp_unclassified
 13:sp.vertebrate 14:sp_virus

Statistics: Mean 46.830; Variance 106.555; scale 0.439

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1375	74.2	212 14	089656	PRE-C/CORE.	2.78e-221
2	1373	74.1	183 14	089437	X, PREC AND C GENES (C	6.51e-221
3	1373	74.1	183 14	068008	X, PREC AND C GENES (F	6.51e-221
4	1374	74.1	212 14	068020	PRE-C/CORE.	4.26e-221
5	1374	74.1	212 14	089597	HBCAG.	4.26e-221
6	1373	74.1	212 14	067876	PRE-C/C ORF.	6.51e-221
7	1372	74.0	212 14	011884	CORE ANTIGEN PRECURSOR	9.96e-221
8	1370	73.9	183 14	068066	X, PREC AND C GENES (L	2.33e-220
9	1370	73.9	212 14	068068	PRE-C/CORE.	2.33e-220
10	1370	73.9	212 14	068025	PRE-C/CORE.	2.33e-220
11	1369	73.8	212 14	067872	PRE-C/C ORF.	3.57e-220
12	1369	73.8	212 14	067884	PRE-C/CORE.	3.57e-220
13	1368	73.8	212 14	068032	PRE-C/CORE.	3.57e-220
14	1368	73.8	212 14	068010	PRE-C/CORE.	5.46e-220
15	1366	73.7	212 14	068070	PRE-C/CORE.	1.28e-219
16	1366	73.7	212 14	068030	PRE-C/CORE.	1.28e-219
17	1364	73.6	183 14	067989	X, PREC AND C GENES (M	2.99e-219
18	1363	73.5	183 14	068048	X, PREC AND C GENES (F	4.57e-219
19	1363	73.5	212 14	068014	PRE-C/CORE.	4.57e-219
20	1363	73.5	212 14	068012	PRE-C/CORE.	4.57e-219

ALIGNMENTS

RESULT ID	1	PRELIMINARY:	PRT:	212 AA.
AC	089656			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)			
DE	PRE-C/CORE.			
GN	PRE-C/CORE.			
OS	HEPATITIS B VIRUS.			
OC	VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-PATIENT LITCHER-1'85;			
RA	LAI M.E., MAZZOLENTI A.P., PORRU A., BALESTRIERI A.;			
RL	SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ATM4;			
RA	PLUCIENNICZAK A.;			
RL	SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	GALBERT F., MANDART E., FITOUSSI F., TIOLLAIS P., CHARNAY P.;			
RL	"Nucleotide sequence of the hepatitis B virus genome (subtype ayw) cloned in E. coli.";			
RT	NATURE 281:646-650(1979).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RA	BORSOVA G.P., PUMPER P.P., BYCHKO V.V., PUSHKO P.M., KALIS Y.V.,			
RL	DISHLER A.V., GREEN E.Y., TSIBINOGIN V.V., KUKAIN R.A.;			
DR	DOKL. BIOCHEM. 279:386-390(1985).			
DR	EMBL: X85290; G736116; -			
DR	EMBL: X85300; G736152; -			
DR	EMBL: X85313; G736196; -			
DR	EMBL: X85283; G736090; -			
DR	EMBL: X85306; G736174; -			
DR	EMBL: X85316; G527437; -			
DR	EMBL: J02203; G329642; -			
DR	EMBL: X85312; G736193; -			
DR	PFAM: PF00906; Hepatitis_core; 1.			
KW	SIGNAL.			
SO	SEQUENCE	212 AA:	24350 MW:	71EAC2C82 CRC32:

Db 209 ESOC 212
245 ESOC 248

RESULT 5
ID 089597 PRELIMINARY: PRT: 212 AA.
AC 089597;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HECAG.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUB-TYPE AYW;
RX MEDLINE: 94079539.
RA PREISLER-ADAMS S., SCHLAYER M.J., PETERS T., HETTLER F., GEROK W.,
RA RASENACK J.;
RT "sequence analysis of hepatitis B virus DNA in immunologically
negative infection";
RL ARCH. VIROL. 133:385-396(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X72702; G288930; -;
DR EMBL: X80925; E198084; -;
DR PRAM: PF00906; Hepatitis_core: 1;
SQ SEQUENCE 212 AA; 24336 MW; 575D20BF CRC32;

Query Match 74.1%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 4,26e-221;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALESPHCSPHHTALRQAI 88
QY :|||||
65 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALESPHCSPHHTALRQAI 124

Db 89 LCMGELMTLATWGVNLEDPASRDVLSYVNTNMGKLFROLMPHISCLTFGRTVIEYL 148
QY :|||||
125 LCMGELMTLATWGVNLEDPASRDVLSYVNTNMGKLFROLMPHISCLTFGRTVIEYL 184

Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 208
QY :|||||
185 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 244

Db 209 ESOC 212
245 ESOC 248

RESULT 6
ID 067876 PRELIMINARY: PRT: 212 AA.
AC 067876;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE C/C ORF.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CI, HBV SUBTYPE AYW;
RA LAI M.E., MAZOLENI A.P., BALESTRIERI A., MELIS A., PORRU A.;

RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65258; G59436; -;
DR PRAM: PF00906; Hepatitis_core: 1;
SQ SEQUENCE 212 AA; 24348 MW; 6ED741BE CRC32;

Query Match 74.1%; Score 1373; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 6,51e-221;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALESPHCSPHHTALRQAI 88
QY :|||||
65 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALESPHCSPHHTALRQAI 124

Db 89 LCMGELMTLATWGVNLEDPASRDVLSYVNTNMGKLFROLMPHISCLTFGRTVIEYL 148
QY :|||||
125 LCMGELMTLATWGVNLEDPASRDVLSYVNTNMGKLFROLMPHISCLTFGRTVIEYL 184

Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 208
QY :|||||
185 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 244

Db 209 ESOC 212
245 ESOC 248

RESULT 7
ID 011884 PRELIMINARY: PRT: 212 AA.
AC 011884;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN PRECURSOR.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA RAO B.S., CASEY J.L., RINAUDO J.S., KOREA B.E.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U95551; G2182120; -;
DR PRAM: PF00906; Hepatitis_core: 1;
SQ SEQUENCE 212 AA; 24360 MW; 73AC92DB CRC32;

Query Match 74.0%; Score 1372; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 9,96e-221;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALESPHCSPHHTALRQAI 88
QY :|||||
65 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALESPHCSPHHTALRQAI 124

Db 89 LCMGELMTLATWGVNLEDPASRDVLSYVNTNMGKLFROLMPHISCLTFGRTVIEYL 148
QY :|||||
125 LCMGELMTLATWGVNLEDPASRDVLSYVNTNMGKLFROLMPHISCLTFGRTVIEYL 184

Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 208
QY :|||||
185 VSEFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSQSPRRRSQSR 244

Db 209 ESOC 212
245 ESOC 248

RESULT 8
ID 068066 PRELIMINARY: PRT: 183 AA.
AC 068066;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X. PREC AND C GENES (LICHERI 2).
GN CORE.
OS HEPATITIS B VIRUS.

OC VIRUSES RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-PATIENT LICHIERI-2'87;
RC LAI M.E., MAZZOLEN A.P., PORRU A., BALESTRIERI A.;
RA SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RL EMBL: X85314 G336204. --
DR FRAM: PF00906; Hepatitis_core: 1
DQ SEQUENCE 183 AA; 21102 MW; 6F38AAB3 CRC32;

Query Match	73.98;	Score 1370;	DB 14;	Length 183;
Best Local Similarity	98.48;	Pred. No. 2.33e-220;		
Matches 180; Conservative	3;	Mismatches 0;	Indels 0;	Gaps 0;

D6		1	MDIDPKFEGATVELLSLPDFFPSVNDLDTASALYRDALSEPSCSHHTLRQAIL	60
OY		66	MDIDPKFEGATVELLSLPDFFPSVRDLDTASALYREALSEPEHCSPHHTLRQAIL	125
D6		61	CWGLMTLATWVGVLNLEDDPASRDLVSVYNTNMGLKFRQLLMFHSICLTFGRETVIEYL	120
OY		126	CWGLMTLATWVGVLNLEDDPASRDLVSVYNTNMGLKFRQLLMFHISICLTFGRETVIEYL	185
D6		121	SFGWIRIPPAIYRPNNAILSTLLETIVYRRRGSTPPRRPSPFKRRRSQSPPRRRSQSRE	180
OY		186	SFGWIRIPPAIYRPNNAILSTLLETIVYRRRGSRPRKRTPSPRRRSQSPPRRRSQSRE	245
D6		181	SQC 183 	
OY		246	SQC 248	

Query Match	73.98;	Score 1370;	DB 14;	Length 212;
Best Local Similarity	98.98;	Pred. No. 2.33e-220;		
Matches 182; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0

Db	29	GMDIDPYKFCATYELLSEFSDSEFPYSRDLDDPASALYRALESPEHCSPHNTALQAI	88
Qy	65	SMDDIPYKFCATYELLSEFSDSEFPYSRDLDDPASALYRALESPEHCSPHNTALQAI	124
Db	89	LCWGEIMLTATWAGVNLDDPASRDLYSVYNTNNGLKFRLQMLFHICLTFTGRTVIEYL	148
Qy	125	LCWGEIMLTATWAGVNLDDPASRDLYSVYNTNNGLKFRLQMLFHICLTFTGRTVIEYL	184
Db	149	VSEGVWITPPAYRPPNPAPILSTLETTVRRRGSRPRRRTPSRRRRSSQSPRRRSQSR	208
Qy	185	VSEGVWITPPAYRPPNPAPILSTLETTVRRRGSRPRRRTPSRRRRSSQSPRRRSQSR	244
Db	209	ESQC 212	
Qy	245	ESQC 248	

AC Q068025;
 DT 01-NOV-1996 (TREMBL.REL. 01, CREATED)
 DT 01-NOV-1996 (TREMBL.REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBL.REL. 08, LAST ANNOTATION UPDATE)
 DE PRE-C/CORE.
 GN PRE-C/CORE.
 OS HEPATITIS B VIRUS.
 CC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PATIENT CASTAG/3;
 RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRERI A.;
 RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: X85293; G736126; -
 DR PFAM: PF00906; HEPATITIS_core: 1.
 SQ SEQUENCE 212 AA, 24363 MW, A6A254DF CRC32;

Query Match	73.9%	Score 1370	DB 14	Length 212
Best Local Similarity	98.9%	Pred. No. 2.33e-220		
Matches 182; Conservative	1	Mismatches 1	Indels 0	Gaps 0

Qy	65	SMDIDPYKEP	EATYELLIS	FLPSDF	FFPSYRDL	DTASALY	KEALES	P	HCSP	HNAL	QAI	124
Db	29	GMDIDPYKEP	EATYELLIS	FLPSDF	FFPSYRDL	DNA	SALYKEALES	P	HCSP	HNAL	QAI	88
	:	:	:	:	:	:	:	:	:	:	:	:
Qy	89	LCWGE	LMTLATW	GVNLED	PASRD	LV	SVYNT	NGKLF	ROLL	MHIS	CLTF	GRTVIEYL
Db	125	LCWGE	LMTLATW	GVNLED	PASRD	LV	SVYNT	NGKLF	ROLL	MHIS	CLTF	GRTVIEYL
Qy	149	VSFGW	IRTP	PAV	RP	NP	PI	SLT	LP	ETV	VR	RGR
Db	185	VSFGW	IRTP	PAV	RP	NP	PI	SLT	LP	ETV	VR	RGR
Qy	209	VSFGW	IRTP	PAV	RP	NP	PI	SLT	LP	ETV	VR	RGR
Db	245	VSFGW	IRTP	PAV	RP	NP	PI	SLT	LP	ETV	VR	RGR
Qy	248	VSFGW	IRTP	PAV	RP	NP	PI	SLT	LP	ETV	VR	RGR

Query Match	73.8%;	Score 1369;	DB 14;	Length 212;
Best Local Similarity	98.4%;	Pred. No. 3.57e-220;		
Matches 181;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;

Db	29	GMDIDPYKEFGATVELLSFLPSDFPSPYRDLDDTAASALYRRALESPEHCSPHHTALRQAI	88
Qy	65	SMDDIPYKEFGATVELLSFLPSDFPSPYRDLDDTAASALYRRALESPEHCSPHHTALRQAI	124
Db	89	LCWGEMLTLAWAGYNLEDDPASRDLYSVYNTNGCLKEFRQLMPEHISCLIFGRETVEIYL	148
Qy	125	LCWGEMLTLAWAGYNLEDDPASRDLYSVYNTNGCLKEFRQLMPEHISCLIFGRETVEIYL	184
Db	149	VSFGEWIRTPTAPYRPNPAPILISTLPETTVVARRGRSPRRRTPSFRRRRSSPPRRRSQSR	206
Qy	185	VSFGEWIRTPTAPYRPNPAPILISTLPETTVVARRGRSPRRRTPSFRRRRSSPPRRRSQSR	244
Db	209	ESQC	212

OY 245 ESQC 248

RESULT 12
ID 067984 PRELIMINARY; PRT: 212 AA.

AC 067984;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.

OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT VITTORINA '92;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85236; G736032; .
PFAM: PF00906; Hepatitis_core: 1.

SO SEQUENCE 212 AA; 24322 MW; 83D9780B CRC32;

Query Match 73.8%; Score 1369; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 3.57e-220;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||

DB 65 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 124
:|||||

OY 89 LCMGELMTLATWGVNEDPASRDVLSYVNTNGLKFRQLMWHISCLTFGRTVIEYL 148
:|||||

DB 125 LCMGELMTLATWGVNEDPASRDVLSYVNTNGLKFRQLMWHISCLTFGRTVIEYL 184
:|||||

OY 149 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||

DB 185 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 244
:|||||

OY 209 ESQC 212
:|||||

DB 245 ESQC 248

RESULT 13
ID 068032 PRELIMINARY; PRT: 212 AA.

AC 068032;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.

OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CHIGLINE-2'86;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85296; G736139; .
PFAM: PF00906; Hepatitis_core: 1.

SO SEQUENCE 212 AA; 24308 MW; 69D87B53 CRC32;

Query Match 73.8%; Score 1369; DB 14; Length 212;
Best Local Similarity 98.4%; Pred. No. 3.57e-220;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||

DB 65 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 124
:|||||

OY 89 LCMGELMTLATWGVNEDPASRDVLSYVNTNGLKFRQLMWHISCLTFGRTVIEYL 148
:|||||

DB 125 LCMGELMTLATWGVNEDPASRDVLSYVNTNGLKFRQLMWHISCLTFGRTVIEYL 184
:|||||

OY 149 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||

DB 185 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 244
:|||||

OY 209 ESQC 212
:|||||

DB 245 ESQC 248

OY 125 LCMGELMTLATWGVNEDPASRDVLSYVNTNGLKFRQLMWHISCLTFGRTVIEYL 184
:|||||

DB 149 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||

OY 185 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 244
:|||||

DB 209 ESQC 212
:|||||

OY 245 ESQC 248

RESULT 14
ID 068010 PRELIMINARY; PRT: 212 AA.

AC 068010;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.

OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT FERRACUTI-2'90;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85285; G736100; .
PFAM: PF00906; Hepatitis_core: 1.

SO SEQUENCE 212 AA; 24292 MW; 04AAD12D CRC32;

Query Match 73.8%; Score 1368; DB 14; Length 212;
Best Local Similarity 98.4%; Pred. No. 5.46e-220;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||

DB 65 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 124
:|||||

OY 89 LCMGELMTLATWGVNEDPASRDVLSYVNTNGLKFRQLMWHISCLTFGRTVIEYL 148
:|||||

DB 125 LCMGELMTLATWGVNEDPASRDVLSYVNTNGLKFRQLMWHISCLTFGRTVIEYL 184
:|||||

OY 149 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||

DB 185 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 244
:|||||

OY 209 ESQC 212
:|||||

DB 245 ESQC 248

RESULT 15
ID 068070 PRELIMINARY; PRT: 212 AA.

AC 068070;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.

OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-PATIENT GIORDO'84;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85316; G736210; .
PFAM: PF00906; Hepatitis_core: 1.

SO SEQUENCE 212 AA; 24376 MW; 80F52D0F CRC32;

Query Match 73.7%; Score 1366; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.28e-219;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db	29	GMDIDPKFPGATVEILLSELPDSDFPSRDLDPTRASALYRALESPPHCSPHNTALROAI	88
Qy	65	SMDDIDPKFPGATVEILLSELPDSDFPSRDLDPTRASALYRALESPPHCSPHNTALROAI	124
Db	89	LCWGLMLTLATWGVNLDPASRDLYVSYVNTNGLKFROLLMWHISCLTFGRVIEYL	148
Qy	125	LCWGLMLTLATWGVNLDPASRDLYVSYVNTNGLKFROLLMWHISCLTFGRVIEYL	184
Db	149	VSGFWITPPAYRPPNPPIILLTPETTVARRRGRSPRRRTPSPRRRRSSPPRRRSQSR	208
Qy	185	VSGFWITPPAYRPPNPPIILLTPETTVARRRGRSPRRRTPSPRRRRSSPPRRRSQSR	244
Db	209	ESOC 212	
Qy	245	ESOC 248	

Search completed: Thu Dec 16 13:04:25 1999
Job time : 103 secs.

US3835-10-38183
MDIDPYKEFGATVELLSFLPSDFPSPVRLDLDITASLLQMDGFPPEHLLVDFLOSMDIDPYKEFGATV
ELLSFLPSDFPSPVRLDLDITASALYREALIESPEHCSPHHTALROAILCQGLMILATWGVNLEDPAASRD
LVSVYNTNMGLKFRQLMFIISCLTFGRETIVIEYLVSGWIRTPAYRPPNADILSTLPETTIVRRRG
RSPRRRTSPRRRRSQSPRRRRSQGRESQCI

 W O R L D
 (TM)

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Msrch-pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 16 13:08:54 1999; MasPar time 11.54 Seconds

Tabular output not generated. 442.105 Million cell updates/sec

Title: >US3835-10-38183
 Description: (1-240) from us3835-10-38183.pep
 Perfect Score: 1796
 Sequence: 1 MDIDPYKFGATVELLSFLP.....RRRSQSPRRRSQSPRESQC 240

Scoring table:
 PAM 150
 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:parts 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 33.355; Variance 174.564; scale 0.191

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1375	76.6	194	32	W50242	Hepatitis B virus pre
2	1375	76.6	212	32	W50250	Hepatitis B virus pre
3	1375	76.6	346	5	R27473	S12/core protein.
4	1363	75.9	184	1	P80959	Hepatitis B virus sub
5	1359	75.7	193	32	W50241	Hepatitis B virus pre
6	1358	75.6	183	32	W50251	Hepatitis B virus p21
7	1353	75.3	183	20	W05044	Hepatitis B virus cor
8	1349	75.1	183	1	R05651	Hepatitis B antigen.
9	1349	75.1	183	5	P00041	Sequence of core anti
10	1344	74.8	397	20	W05048	Plasmodium falciparum
11	1338	74.5	184	5	P00004	Sequence of core anti
12	1336	74.4	196	8	R40806	Hepatitis B core / PV
13	1337	74.4	208	8	R40808	Hepatitis B core / PV
14	1334	74.3	183	31	P40311	Hepatitis B virus core
15	1334	74.3	183	8	R40805	Hepatitis B core prot
16	1334	74.3	183	13	R68868	Hepatitis B virus pol

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description	Pred. No.
1	W50242	1375	76.6	194	32	W50242	Hepatitis B virus pre
2	W50242	1375	76.6	212	32	W50250	Hepatitis B virus pre
3	W50242	1375	76.6	346	5	R27473	S12/core protein.
4	W50242	1363	75.9	184	1	P80959	Hepatitis B virus sub
5	W50242	1359	75.7	193	32	W50241	Hepatitis B virus pre
6	W50242	1358	75.6	183	32	W50251	Hepatitis B virus p21
7	W50242	1353	75.3	183	20	W05044	Hepatitis B virus cor
8	W50242	1349	75.1	183	1	R05651	Hepatitis B antigen.
9	W50242	1349	75.1	183	5	P00041	Sequence of core anti
10	W50242	1344	74.8	397	20	W05048	Plasmodium falciparum
11	W50242	1338	74.5	184	5	P00004	Sequence of core anti
12	W50242	1336	74.4	196	8	R40806	Hepatitis B core / PV
13	W50242	1337	74.4	208	8	R40808	Hepatitis B core / PV
14	W50242	1334	74.3	183	31	P40311	Hepatitis B virus core
15	W50242	1334	74.3	183	8	R40805	Hepatitis B core prot
16	W50242	1334	74.3	183	13	R68868	Hepatitis B virus pol

1
 28-SEP-1998 (first entry)
 Hepatitis B virus precore p22 polypeptide Met-p22.
 Viral replication: Inhibitor: HBV, nucleocapsid; gene therapy:
 Hepatocyte; liver; Met-p22.
 Hepatitis B virus.
 Synthetic.
 Location/Qualifiers
 2..194
 /label= p22
 W09809649-A1.
 12-MAR-1998.
 03-SEP-1997; U15500.
 (GENO) GEN HOSPITAL CORP.
 Melegari M, Scaglioni P, Wands JR;
 JPT: 98-193325/17.
 DNA encoding proteins which can be incorporated with wild type
 nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 inhibition of viral replication, especially hepatitis B virus
 Claim 11: Page 40; 60pp; English.
 This polypeptide comprises the hepatitis B virus (HBV) p22
 protein with an added N-terminal Met residue. p22 is produced by
 elimination of the 19-amino acid leader peptide from the 25 kDa
 full-length HBV precore protein (see W50250). Evidence is provided
 that HBV replication is inhibited in the presence of high levels of
 HBV precore or precore-related proteins. These proteins can be
 incorporated into HBV nucleocapsids along with the p21 core protein
 (see W50251), which is the usual nucleocapsid component, and
 thereby render the nucleocapsids deficient in encapsidating HBV
 pregenomic RNA. Thus, over-expression of the precore proteins, or
 certain variants of them, leads to transdominant inhibition of HBV
 replication. Suitable inhibitory proteins include p25 (see W50250),
 p22, Met-p22, p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
 (see W50238). Heterologous peptides (see W50244-49) may be
 inserted into the p22 and Met-p22 polypeptides. The inhibitory
 proteins can be produced by recombinant methods using claimed
 expression vectors and host cells. They can be provided exogenously

CC to the target cells for use in inhibiting HBV replication.
 CC Alternatively, a nucleic acid construct that directs overexpression
 CC of an inhibitory protein in target cells is used for the gene
 CC therapy of HBV infection.
 SQ Sequence 194 AA;

Query Match 76.6%; Score 1375; DB 32; Length 194;
 Best Local Similarity 99.5%; Pred. No. 6.00e-99;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 gmdidpykfeafatvellsfipdsffsvrldlftasalyrealsepncsphtalrqa1 70
 |||||||
 QY 57 SMDIDPKFEAFATVELLSFIPDSFFSVRDLDLTASALIRALSPENCSPHHTALRKQAI 116

Db 71 lwcgelmrlatwgvnledpasrdlsvsvyntmgk1kfrrl1wfhisc1fgretvley1 130
 |||||||
 QY 117 LCMGELMTLATWGVNLEDPASRDLSVSVYNTMGK1KROLMTFHISCLTGFRETVEYL 176
 Db 131 vsfgvwtppayrppnapilstipettvrrrgsprrrrrsgsprrrrrsgsr 190
 |||||||
 QY 177 VSFGVWIRTPPAYRPPNAPILSTIPETTVRRRGSPRRRRSPRRRSQSPRRRSQSR 236

Db 191 esgc 194
 |||||
 QY 237 ESQC 240

RESULT 2
 ID W50250 standard; Protein; 212 AA.
 AC W50250;

DE Hepatitis B virus (first entry)
 KM Hepatitis B virus precore p25 polypeptide.
 KM Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
 KM hepatocyte; liver; p25 protein.

OS Hepatitis B virus.
 PN W09808648-A1.

PD 12-MAR-1998.
 PF 03-SEP-1997; U15500.

PR 03-SEP-1996; US-025370.
 PA (GEHO) GEN HOSPITAL CORP.

PI Melagari M, Scaglioni PR, Wands JR;
 DR WPI; 98-193325/17.

PT DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus
 PS Claim 15; Page 35; 60pp; English.

CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)
 CC protein that is encoded by the full-length HBV precore gene.

CC Evidence is provided that HBV replication is inhibited in the
 CC presence of high levels of HBV precore or precore-related proteins.

CC These proteins can be incorporated into HBV nucleocapsids along
 CC with the p21 core protein (see W50251), which is the usual

CC nucleocapsid component, and thereby render the nucleocapsids
 CC deficient in encapsidating HBV pregenomic RNA. Thus, over-

CC expression of the precore proteins, or certain variants of them,
 CC leads to transdominant inhibition of HBV replication. Suitable

CC inhibitory proteins include p25, p22 (see W50241), Met-p22 (see
 CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het

CC (see W50238). The inhibitory proteins can be produced by
 CC recombinant methods using claimed expression vectors and host

CC cells. They can be provided exogenously to the target cells for
 CC use in inhibiting HBV replication. Alternatively, a nucleic acid

CC construct that directs overexpression of an inhibitory protein in
 CC target cells is used for the gene therapy of HBV infection.

CC Sequence 212 AA;

Query Match 76.6%; Score 1375; DB 32; Length 212;
 Best Local Similarity 99.5%; Pred. No. 6.00e-99;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 gmdidpykfeafatvellsfipdsffsvrldlftasalyrealsepncsphtalrqa1 88
 |||||||
 QY 57 SMDIDPKFEAFATVELLSFIPDSFFSVRDLDLTASALIRALSPENCSPHHTALRKQAI 116

Db 89 lwcgelmrlatwgvnledpasrdlsvsvyntmgk1kfrrl1wfhisc1fgretvley1 148
 |||||||
 QY 117 LCMGELMTLATWGVNLEDPASRDLSVSVYNTMGK1KROLMTFHISCLTGFRETVEYL 176

Db 149 vsfgvwtppayrppnapilstipettvrrrgsprrrrrsgsprrrrrsgsr 208
 |||||||
 QY 177 VSFGVWIRTPPAYRPPNAPILSTIPETTVRRRGSPRRRRSPRRRSQSPRRRSQSR 236

Db 209 esgc 212
 |||||
 QY 237 ESQC 240

RESULT 3
 ID R27473 standard; Protein; 346 AA.
 AC R27473;

DE 24-FEB-1993 (first entry)

KM Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
 KM Hepatitis B virus; 13L; promoter; NYVAC; recombinant; HBV L;

KM large pre-S antigen; spsAg; fusion protein; pre-S region; S12/core;
 KM S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;

KM deletion loci; recipient loci.

OS Synthetic.
 FH Key

FT region
 FT 1..108
 FT /label S1

FT region
 FT 109..163
 FT /label S2

FT region
 FT 164..346
 FT /label Core

PN W09215672-A.

PD 17-SEP-1992.

PF 09-MAR-1992; U01906.
 PR 07-MAR-1991; US-666056.

PR 11-JUN-1991; US-713967.
 PR 06-MAR-1992; US-847951.

PA (VIRO-) VIROGENETICS CORP.
 COX WI, De Taisne C, Francis J, Gettig RR, Johnson GP,

PI Lambach KJ, Norton EK, Paolletti E, Perkins ME, Pincus SE,
 PI Riviere M, Tartaglia J, Taylor J;

DR WPI; 92-331718/40.

DR WPI; 92-331718/40.

PT Vaccine comprises recombinant, attenuated pox-virus - use for
 PT vaccinating against viral infections such as rabies, hepatitis B,

PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure; Fig 13; 45pp; English.

CC The sequence given is encoded by an expression cassette which
 CC comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/
 CC core) which is precisely linked to the 13L promoter derived from

CC vaccinia virus. This DNA sequence was linked to the S1 and S2
 CC sequences and this fragment was used in the construction of a NYVAC

CC recombinant expressing the HBV gene. Other HBV genes were also used
 CC in the construction. These were HBV M protein (small pre-S antigen,

CC spsAg) and HBV L (large pre-S antigen, lpsAg). Each of these gene
 CC sequences were inserted individually into three different sites of

CC NYVAC separated by from each other by large regions of vaccinia DNA
 CC containing essential genes. NYVAC is a Copenhagen vaccine strain of

CC vaccinia virus which has been modified by deletion of six non-essential
 CC regions of the genome encoding known or potential virulence factors.

CC The deletion loci were engineered as recipient loci for the insertion
 CC of foreign genes. The spacing of the three inserted sequences ensured

CC that any recombination that did occur would lead to disruption of the
 CC vaccinia genome and would cause unviable vaccinia virus. See also

CC Q35501-864.
 SQ Sequence 346 AA;

Query Match 76.6%; Score 1375; DB 5; Length 346;
 Best Local Similarity 99.5%; Pred. No. 6.00e-99;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 163 nmdidpykfeafatvellsfipdsffsvrldlftasalyrealsepncsphtalrqa1 222

```

QY 57 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 116
DB 223 LCGWGLMTLATWGVNLDPSARDLVSVYNTNMGLKFRQLVFNHSCITFFGREVIEYL 282
QY 117 LCGWGLMTLATWGVNLDPSARDLVSVYNTNMGLKFRQLVFNHSCITFFGREVIEYL 176
DB 283 VSFQWITPPAYRPPNAPILSTLPETVVRIRGRSPRRTRSPRRRSQSPRRRSQSR 342
QY 177 VSFQWITPPAYRPPNAPILSTLPETVVRIRGRSPRRTRSPRRRSQSPRRRSQSR 236
DB 343 ESQC 346
QY 237 ESQC 240

RESULT 4
ID P80959 standard; protein: 184 AA.
AC P80959;
DT 19-NOV-1990 (first entry)
DE Hepatitis B virus subtype ayw. core protein.
KM Conjugate; fusion protein; hepatitis B core protein; HBV subtype ayw.;
  T cell stimulating polypeptide; vaccines.
OS Synthetic.
PN EP-271302-A.
PD 15-JUN-1988.
PF 07-DEC-1987; 310725.
PR 07-OCT-1987; US-106538.
PR 07-OCT-1987; US-939617.
PA (SCRT-) Scripps Clinic Res.
PI Thornton GB, Mortuary AM, Millich DR, McLachlan A.;
DR WPI: 88-163287/24.
PT New conjugates and fusion proteins of immunogenic polypeptide -
  PT and hepatitis B core antigen and T cell stimulating polypeptide
  corep. to core antigen, useful in vaccines.
PS Disclosure: P. English.
CC This sequence contains the T cell stimulating epitopes, amino acid
  CC residue 1-55 and 70-140. It is believed that the regions 1-44 and
  CC 70-140 do not contain determinants that suppress T cell activation.
  CC Polypeptides essentially consisting of 15 to 55 amino acids
  CC corresponding to the above mentioned HBV regions are T cell
  CC stimulating. Coupling a polypeptide immunogen to such sequences,
  CC e.g. by using a bifunctional reagent which forms a disulphide link,
  CC improves its immunogenicity. These are useful in vaccines and can be used
  CC therapeutically to improve T cell response to HBcAg in infected
  CC subjects.
CC See also P80896-P80898 and P80951-P80859.
SQ Sequence 184 AA;

Query Match 75.9%; Score 1363; DB 1; Length 184;
Best Local Similarity 99.5%; Pred. No. 5, 67e-98;
Matches 183; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 10 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 69
QY 57 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 116
DB 70 LCGWGLMTLATWGVNLDPSARDLVSVYNTNMGLKFRQLVFNHSCITFFGREVIEYL 129
QY 117 LCGWGLMTLATWGVNLDPSARDLVSVYNTNMGLKFRQLVFNHSCITFFGREVIEYL 176
DB 130 VSFQWITPPAYRPPNAPILSTLPETVVRIRGRSPRRTRSPRRRSQSPRRRSQSR 189
QY 177 VSFQWITPPAYRPPNAPILSTLPETVVRIRGRSPRRTRSPRRRSQSPRRRSQSR 236
DB 190 ESQC 193
QY 237 ESQC 240

RESULT 6
ID W50251 standard; protein: 183 AA.
AC W50251;
DT 28-SEP-1998 (first entry)
DE Hepatitis B virus p21 core protein.
KM Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
  KM hepatocyte; liver; p21; core protein.
OS Hepatitis B virus.
FT Key Location/Qualifiers
  FT 82..98
  FT /note="Immunodominant region"
  PN W09809649-A1.
  PD 12-MAR-1998.
  PF 03-SEP-1997; U15500.
  PR 03-SEP-1996; US-025370.
  PA (GEO) GEN HOSPITAL CORP.
  PI Melegari M, Scaglioni PP, Wands JR;
  DR WPI: 98-193325/17.
  PT DNA encoding proteins which can be incorporated with wild type
  PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
  PT inhibition of viral replication, especially hepatitis B virus
  PS Claim 9; Page 34-35; 60pp; English.
  CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
  CC peptide from the 25 kDa full-length HBV precore protein (see
  CC W50250). Evidence is provided that HBV replication is inhibited in
  CC the presence of high levels of HBV precore or precore-related
  CC proteins. These proteins can be incorporated into HBV nucleocapsids
  CC along with the p21 core protein (see W50251), which is the usual
  CC nucleocapsid component, and thereby render the nucleocapsids
  CC deficient in encapsidating HBV pregenomic RNA. Thus, over-
  CC expression of the precore proteins, or certain variants of them,
  CC leads to transdominant inhibition of HBV replication. Suitable
  CC inhibitory proteins include p25 (see W50250), p22, Met-p22 (see
  CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
  CC (see W50238). Heterologous peptides (see W50244-49) may be
  CC inserted into the p22 and Met-p22 polypeptides. The inhibitory
  CC proteins can be produced by recombinant methods using claimed
  CC expression vectors and host cells. They can be provided exogenously
  CC to the target cells for use in inhibiting HBV replication.
  CC Alternatively, a nucleic acid construct that directs overexpression
  CC of an inhibitory protein in target cells is used for the gene
  CC therapy of HBV infection.
  SQ Sequence 193 AA;

Query Match 75.7%; Score 1359; DB 32; Length 193;
Best Local Similarity 98.4%; Pred. No. 1, 20e-97;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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PF 1-JAN-1989; 123526.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOI) Biogen Inc.
PI Murray K. Schaller HE;
DR WPI: 90-195067/26.
N-PSDB: 004799
PT Recombinant DNA encoding Hepatitis B virus polypeptide antigens -
PS used in detection of infection and in vaccine prodn.
CC Polypeptide fragments encoded by the DNA sequence are antigenic for
CC HBV and may be used as a vaccine or in detection. Peptides may be
CC cultured in a suitable bacterial host such as E.coli.
CC Fragments of the sequence are also claimed as being antigenically
CC useful.
SQ Sequence 183 AA;

Query Match 75.1%; Score 1349; DB 1; Length 183;
Best Local Similarity 96.7%; Pred. No. 7.78e-97;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdidpykefatvellsflpsdffsvrrdlldaalyrdlaespehscphthalrga11 60
|||||
QY 58 MDIDPYKEFATVLLSFLPSDFPSVRDLDTASALYREALSPESHCSPHHTALRQA1L 117
Db 61 cwgdlmclatwgvnldpsardlvsvyvtmnglkfrqllwfhsccltfgretvleylv 120
|||||
QY 118 CWGELMTLATWGVNLDPSARDLVSVYVTNMGLKRFQLLMFHISCLTFRGRETIVIELV 177
Db 121 sfgywltppayrpnaplslpctvrrrrgrsprrrrrpsrrrrsgsre 180
|||||
QY 178 SFGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSRRRSQSRE 237
Db 181 sqc 183
|||
QY 238 SQC 240

RESULT 9
ID P00041 standard; Protein; 183 AA.
AC P00041;
DT 14-OCT-1992 (first entry)
DE Sequence of core antigen.
KM Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
OS Hepatitis B virus.
PN EP-13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979; 303017.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOI) BIOGEN NV.
PI Murray K. Schaller HE;
DR WPI: 80-57268C/33.
N-PSDB: N00003.
PT Recombinant DNA coding for polypeptide - have specificity of
PT hepatitis B viral antigens in detection or antibody stimulation
PS Example: Figs 3-4; 43pp; English.
CC Human serum from a single HBsAg positive, HBsAg positive donor
CC (serotype adym) was used to prep. a DNA-contg. pellet which was
CC labelled with 3H or 32P as described by P. M. Kaplan et al (1973).
CC The labelled DNA was then extracted with phenol from the resulting
CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
CC It was then cloned in plasmid pBR322 which was used to transform E.
CC coli. Micro-organisms prepd. by the processes are deposited at the
CC NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dg:
ID HBV-Kpn I dg: Tetr Amps HBV+.
SQ Sequence 183 AA;

Query Match 75.1%; Score 1349; DB 5; Length 183;
Best Local Similarity 96.7%; Pred. No. 7.78e-97;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdidpykefatvellsflpsdffsvrrdlldaalyrdlaespehscphthalrga11 60
|||||
QY 58 MDIDPYKEFATVLLSFLPSDFPSVRDLDTASALYREALSPESHCSPHHTALRQA1L 117
Db 61 cwgdlmclatwgvnldpsardlvsvyvtmnglkfrqllwfhsccltfgretvleylv 120
|||||
QY 118 CWGELMTLATWGVNLDPSARDLVSVYVTNMGLKRFQLLMFHISCLTFRGRETIVIELV 177
Db 121 sfgywltppayrpnaplslpctvrrrrgrsprrrrrpsrrrrsgsre 180
|||||
QY 178 SFGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSRRRSQSRE 237
Db 181 sqc 183
|||
QY 238 SQC 240

RESULT 10
ID W09048 standard; Protein; 397 AA.
AC W09048;
DT 11-APR-1997 (first entry)
DE Plasmid pHBV DN AA encoded HBV dominant negative polypeptide.
KM Hepadnavirus; woodchuck hepatitis virus; hepatitis delta virus;
KM HBV; ground squirrel hepatitis B virus; duck hepatitis B virus;
KM core protein; replication; antiviral; gene therapy; pHBV DN AA.
OS Hepatitis B virus.
FH Key location/Qualifiers
FT region 1..179
FT /label= HBV-core
FT /note= "positions 1-179 correspond to amino acids
FT 1-179 of HBV core protein"
FT region 180..397
FT /note= "positions 180-397 correspond to amino
FT acids 9-226 of HBV surface protein"

PN W09700698-A1.
PD 09-JAN-1997.
PF 20-JUN-1996; U10602.
PR 20-JUN-1995; US-017814.
PA (GEHO) GEN HOSPITAL CORP.
PI Melegari M, Scaglioni PP, Wands JR;
DR WPI: 97-087176/08.
N-PSDB: T49598.
PT New method for inhibiting the replication of hepadnaviruses -
PT comprises introducing a mutant polypeptide with a mutated core
PT protein or corresponding nucleic acid, for treating, e.g. hepatitis
PT B
PS Disclosure; Page 46-48; 83pp; English.
CC Plasmid pHBV DN AA carries an insert (T49598) coding for a protein
CC (W09048) comprising a hepatitis B virus (HBV) core protein (see
CC also W09044) fused in-frame at amino acid 179 with the HBV surface
CC protein (see also W09045) at amino acid 8. Plasmid pHBV DN BB
CC (T49599) expresses the HBV core fused at amino acid 175 to the
CC surface protein at amino acid 112 (W09049). pHBV DN AA was at
CC least as potent an inhibitor of HBV replication as construct
CC pHBV DN (T49597); pHBV DN BB was less inhibitory than pHBV DN.
CC Vectors expressing hepadnavirus dominant negative core mutants can
CC be utilised in the gene therapy of viral infections.
SQ Sequence 397 AA;

Query Match 74.8%; Score 1344; DB 20; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.98e-96;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mdidpykefatvellsflpsdffsvrrdlldaalyrdlaespehscphthalrga11 60
|||||
QY 58 MDIDPYKEFATVLLSFLPSDFPSVRDLDTASALYREALSPESHCSPHHTALRQA1L 117
Db 61 cwgdlmclatwgvnldpsardlvsvyvtmnglkfrqllwfhsccltfgretvleylv 120
|||||
QY 118 CWGELMTLATWGVNLDPSARDLVSVYVTNMGLKRFQLLMFHISCLTFRGRETIVIELV 177
Db 121 sfgywltppayrpnaplslpctvrrrrgrsprrrrrpsrrrrsgsre 179

Query 178 SFGWIRTPPAIRPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 236

RESULT 11
ID P00004 standard; Protein: 184 AA.

AC P00004;
DT 14-OCT-1992 (first entry)
DE Sequence of core antigen.
KW Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
OS Hepatitis B virus.

PN EP-13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979; 303017.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOJ) BIOGEN NV.
PI Murray K, Schaller HE.
DR WPI: 80-57268C/33.
DR N-PSDB: N00002.
PT Recombinant DNA coding for polypeptide - have specificity of
PS hepatitis B viral antigens in detection or antibody stimulation

Claim 13: Page 40; 43pp: English.
CC Human serum from a single HBsAg positive, HBeAg positive donor
CC (serotype adym) was used to prep. a DNA-contg. pellet which was
CC labelled with 3H or 32P as described by P. M. Kaplan et al (1973).
CC The labelled DNA was then extracted with phenol from the resulting
CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
CC It was then cloned in plasmid pBR322 which was used to transform E.
CC coli. Micro-organisms prep'd. by the processes are deposited at the
CC NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst 1 dg:
CC HBV-kpn I dc: Tetr Amps HBV+.
SQ Sequence 184 AA;

Query Match 74.5%; Score 1338; DB 5; Length 184;

Best Local Similarity 96.2%; Pred. No. 6.09e-96;

Matches 177; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

DB 1 mdidpykefgatvellslfspdffpsvcrdlldtaaalysdalespeshphthalrgai 60
QY 58 MODIDPYKEFGATVELLSFLPSDFPSV-RDLDTASALYREALSEPHCHPHHTALRQAI 116
DB 61 lcgwdlmlatwvgnledpasrdlvsyvnmgjklrqlwfhiscitfgretvleyl 120
QY 117 LCGWELMTLATWGVNLEDPASRDLVSYVNTMGLKFRQLMFHISCITFGRETVEYL 176
DB 121 vsfgvwtirppayrpnnapilslptetvvrgrgsprrrtsprrrrsgsr 180
QY 177 vsfgvwtirppayrpnnapilslptetvvrgrgsprrrtsprrrrsgsr 236
DB 181 esgc 184
QY 237 ESQC 240

RESULT 12
ID R40806 standard; Protein: 196 AA.

AC R40806;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 fusion.
KW Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Synthetic.

FN Key Location/Qualifiers
FT region 7..13
FT protein /label= PV-1
FT protein /label= HBC

PN J05192170-A.
PD 03-AUG-1993.
PF 24-SEP-1991; 243800.
PR 24-SEP-1991; JP-243800.
PA (NISM) NISSHIN OIL MILLS LTD. ?

DR WPI: 93-277479/35.

DR N-PSDB: Q47736.

PT Recombinant plasmid for high immunogenicity virus - contains
PT Recombinant haemagglutinin gene, hepatitis B core gene of vaccinia
PT virus and exotic genes

PS Disclosure: Fig 7; 12pp; Japanese.
CC The hepatitis B core gene is recombined with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.
SQ Sequence 196 AA;

Query Match 74.4%; Score 1336; DB 8; Length 196;

Best Local Similarity 95.1%; Pred. No. 8.86e-96;

Matches 175; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

DB 13 andidpykefgasvellslfspdffpsvcrdlldtaaalysdalespeshphthalrgai 72
QY 57 SMDIDPYKEFGATVELLSFLPSDFPSVCRDLDTASALYREALSEPHCHPHHTALRQAI 116
DB 73 lcgwdlmlatwvgnledpasrdlvsyvnmgjklrqlwfhiscitfgretvleyl 132
QY 117 LCGWELMTLATWGVNLEDPASRDLVSYVNTMGLKFRQLMFHISCITFGRETVEYL 176
DB 133 vsfgvwtirppayrpnnapilslptetvvrgrgsprrrtsprrrrsgsr 192
QY 177 vsfgvwtirppayrpnnapilslptetvvrgrgsprrrtsprrrrsgsr 236
DB 193 esgc 196
QY 237 ESQC 240

RESULT 13
ID R40808 standard; Protein: 208 AA.

AC R40808;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 / IL-1 fusion.
KW Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Synthetic.

FN Key Location/Qualifiers
FT region 8..19
FT protein /label= PV-1
FT protein /label= IL-1
FT protein /label= HBC

PN J05192170-A.
PD 03-AUG-1993.
PF 24-SEP-1991; 243800.
PR 24-SEP-1991; JP-243800.
PA (NISM) NISSHIN OIL MILLS LTD.
DR WPI: 93-277479/35.

DR N-PSDB: Q47738.
PT Recombinant plasmid for high immunogenicity virus - contains
PT recombined haemagglutinin gene, hepatitis B core gene of vaccinia
PT virus and exotic genes
PS Disclosure: Fig 9; 12pp; Japanese.
CC The hepatitis B core gene is recombined with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.
SQ Sequence 208 AA;

Query Match 74.4%; Score 1337; DB 8; Length 208;

Best Local Similarity 94.6%; Pred. No. 7.35e-96;

Matches 175; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

DB 24 lcgwdlmlatwvgnledpasrdlvsyvnmgjklrqlwfhiscitfgretvleyl 83
QY 56 LSGWELMTLATWGVNLEDPASRDLVSYVNTMGLKFRQLMFHISCITFGRETVEYL 115
DB 84 lcgwdlmlatwvgnledpasrdlvsyvnmgjklrqlwfhiscitfgretvleyl 143

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QY 116 ILCWGELMTLATVGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETVEY 175
DB 144 lvsfgwlrtpayrppnapilslpettivrigrsprrrpsrrrrsgsrrrrsgs 203
QY 176 LVSFGWLRTPPAYRPPNAPILSLPETTVVRRGRSPRRRTSPRRRSQSRRRSQS 235
DB 204 resqc 208
QY 236 RESQC 240

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RESULT 14
ID P40311 standard: Protein: 183 AA.
AC P40311:
DE 18-AUG-1992 (first entry)
DE Hepatitis virus core antigen.
KM HBcAg: vaccine; diagnosis; HBV infection.
OS Hepatitis B virus.
PN J59074985-A.
PD 27-APR-1984.
PF 19-OCT-1982; 183432.
PF 19-OCT-1982; JP-183432.
PA (TAKE ) TAKEDA CHEMICAL IND KK.
DR WPI: 84-143231/23.
PT DNA used in prevention of infections by hepatitis virus B -
PT comprises structural gene of hepatitis virus adr B surface antigen
PS coding gene and at least 1 virus core antigen structural gene.
PS Disclosure: Fig 3: 13pp; Japanese.
CC The sequence is that of hepatitis virus core antigen (HBcAg). It
CC can be used as a vaccine for the prevention of infections by
CC hepatitis B virus (HBV) and also in the diagnosis of early stages
CC of HBV infection. See also P40310.
SQ Sequence 183 AA:

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Query Match 74.3%: Score 1334; DB 4; Length 183;
Best Local Similarity 95.6%: Pred. No. 1.29e-95;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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DB 1 mdidpykefgasvellsfipdsdfpsirdltdasalyrealaspehcsphhtalrga11 60
QY 58 MDIDPYKEFGATVELLSFLPSDFPSRDLDTASALYREALSPHCHSPTHALRQAIL 117
DB 61 cwgelmjlatwvgsnledpasrelvsvyvnmgklkrlqlwfhisccltfgrtveleylv 120
QY 118 CWGELMTLATVGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETVEYLV 177
DB 121 sfvgwlrtpayrppnapilslpettivrigrsprrrpsrrrrsgsrrrrsgsre 180
QY 178 SFGWLRTPPAYRPPNAPILSLPETTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 237
DB 181 sqc 183
QY 238 SQC 240

```

```

RESULT 15
ID R40805 standard: Protein: 183 AA.
AC R40805:
DE 16-FEB-1994 (first entry)
DE Hepatitis B core protein.
KM Hepatitis B: core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Hepatitis B virus.
PN J05192170-A.
PD 03-AUG-1993.
PF 24-SEP-1991; 243800.
PF 24-SEP-1991; JP-243800.
PA (NISW ) NISSHIN OIL MILLS LTD.
DR N-PDB: Q47735.
PT Recombinant plasmid for high immunogenity virus - contains
PT recombined haemagglutinin gene, hepatitis B core gene of vaccinia
PT virus and exotic genes

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PS Disclosure: Fig 6: 12pp; Japanese.
CC The hepatitis B core gene is recombinant with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.
SQ Sequence 183 AA:

```

```

Query Match 74.3%: Score 1334; DB 8; Length 183;
Best Local Similarity 95.6%: Pred. No. 1.29e-95;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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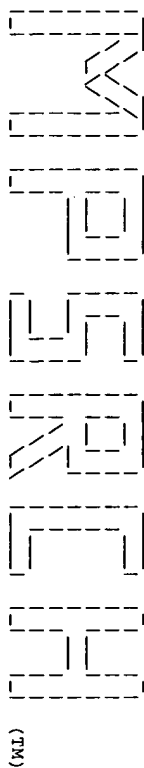
DB 1 mdidpykefgasvellsfipdsdfpsirdltdasalyrealaspehcsphhtalrga11 60
QY 58 MDIDPYKEFGATVELLSFLPSDFPSRDLDTASALYREALSPHCHSPTHALRQAIL 117
DB 61 cwgelmjlatwvgsnledpasrelvsvyvnmgklkrlqlwfhisccltfgrtveleylv 120
QY 118 CWGELMTLATVGVNLEDPASRDVSVYNTNMGLKFRQLMFHISCLTFGRETVEYLV 177
DB 121 sfvgwlrtpayrppnapilslpettivrigrsprrrpsrrrrsgsrrrrsgsre 180
QY 178 SFGWLRTPPAYRPPNAPILSLPETTVVRRGRSPRRRTSPRRRSQSRRRSQSRE 237
DB 181 sqc 183
QY 238 SQC 240

```

```

Search completed: Thu Dec 16 13:11:36 1999
Job time : 162 secs.

```

(TM)

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MPsrch_p protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 13:11:54 1999; Maspar time 12.41 Seconds
775.040 Million cell updates/sec
Tabular output not generated.

Title: >US3835-10-38183
Description: (1-240) from us3835-10-38183.pep
Perfect Score: 1796
Sequence: 1 MDIDPKKFGATVELLSFLP.....RRRSQSPRRRRSQSRESQC 240

Scoring table:
PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r60
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 47.190; Variance 119.785; scale 0.394

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1375	76.6	212	1	NKVLAH e antigen precursor / 4.47e-198	
2	1374	76.5	212	2	S53211 e antigen precursor / 6.55e-198	
3	1374	76.5	212	2	S53204 e antigen precursor / 6.55e-198	
4	1373	76.4	183	2	S53207 core antigen - hepati / 9.59e-198	
5	1373	76.4	212	2	S520750 e antigen precursor / 3.01e-197	
6	1370	76.3	183	2	S53216 e antigen precursor / 3.01e-197	
7	1370	76.3	212	2	S53216 e antigen precursor / 3.01e-197	
8	1370	76.3	212	2	S53216 e antigen precursor / 3.01e-197	
9	1369	76.2	212	2	S53163 e antigen precursor / 4.40e-197	
10	1369	76.2	212	2	S53163 e antigen precursor / 4.40e-197	
11	1369	76.2	212	2	S53225 e antigen precursor / 4.40e-197	
12	1368	76.2	212	2	S53198 e antigen precursor / 6.45e-197	
13	1366	76.1	212	2	S53223 e antigen precursor / 1.38e-196	
14	1366	76.1	212	2	S53223 e antigen precursor / 1.38e-196	
15	1364	75.9	183	2	S53169 core antigen - hepati / 2.96e-196	
16	1363	75.9	183	2	S53247 core antigen - hepati / 4.33e-196	
17	1363	75.9	212	2	S53202 e antigen precursor / 4.33e-196	
18	1363	75.9	212	2	S53159 e antigen precursor / 4.33e-196	
19	1363	75.9	212	2	S53200 e antigen precursor / 4.33e-196	
20	1362	75.8	212	2	S53251 e antigen precursor / 6.34e-196	
21	1360	75.7	212	2	S53204 e antigen precursor / 1.36e-195	
22	1360	75.7	212	2	S53227 e antigen precursor / 1.36e-195	
23	1359	75.7	212	2	S53233 e antigen precursor / 1.99e-195	

24	1358	75.6	211	1	NKVLAI e antigen precursor / 2.91e-195
25	1357	75.6	212	2	S53281 e antigen precursor / 4.26e-195
26	1355	75.4	212	1	NKVLBH e antigen precursor / 9.13e-195
27	1355	75.4	212	2	S53242 e antigen precursor / 9.13e-195
28	1351	75.2	183	2	S53129 core antigen - hepati / 4.19e-194
29	1351	75.2	212	2	S53240 e antigen precursor / 4.19e-194
30	1349	75.1	183	1	NKVLAI2 e antigen - hepati / 8.98e-194
31	1349	75.1	183	2	S53181 e antigen - hepati / 8.98e-194
32	1348	75.1	183	2	S53232 e antigen - hepati / 1.31e-193
33	1348	75.1	183	2	S53260 e antigen - hepati / 1.31e-193
34	1345	74.9	183	2	S53152 core antigen - hepati / 4.12e-193
35	1343	74.8	183	2	S53214 core antigen - hepati / 8.83e-193
36	1344	74.8	212	2	S53229 e antigen precursor / 6.03e-193
37	1342	74.7	183	2	S53140 e antigen - hepati / 1.29e-192
38	1341	74.7	183	2	S53267 core antigen - hepati / 1.89e-192
39	1341	74.7	183	2	S53189 core antigen - hepati / 1.89e-192
40	1341	74.7	212	2	S53238 e antigen precursor / 1.89e-192
41	1339	74.6	183	2	S53157 core antigen - hepati / 4.05e-192
42	1340	74.6	212	2	S53257 e antigen precursor / 2.77e-192
43	1339	74.6	212	2	S25651 e antigen precursor / 4.05e-192
44	1338	74.5	212	2	S53236 e antigen precursor / 5.93e-192
45	1337	74.4	212	1	NKVLJ2 e antigen precursor / 8.68e-192

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE NKVLAH #type complete
e antigen precursor / core antigen - hepatitis B virus
(subtype ayw4, isolate hb321 and others)
HBE antigen precursor / Hbc antigen; pre-C/C antigen
CONTAINS
core antigen; e antigen
ORGANISM
#variety
#formal_name hepatitis B virus, HBV
subtype ayw4, isolate hb321; isolate patient Ferracuti '83;
isolate patient Castag '83; isolate patient Sanna '84;
isolate patient Licheri '1-85; isolate patient Flore '1-86;
isolate patient Licheri '83
18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change
10-Oct-1997
DATE S47405; S53191; S53209; S53234; S53264; S53249; S53262;
S53277; A03711
ACCESSIONS
REFERENCE S47404
#authors Plucieniczak, A.
#submission submitted to the EMBL Data Library, August 1994
#description Molecular cloning and sequencing of two complete genomes of
Polish isolates of human hepatitis B virus.
#accession S47405
#molecule_type DNA
#residues 1-212 #label PLU
##cross-references EMBL:235116; NID:q527435; PID:q527437
REFERENCE S53112
#authors Lal, M.E.; Mazzoleni, A.P.; Portu, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53191
#molecule_type DNA
#residues 1-212 #label LA1
##cross-references EMBL:X85283; NID:q736088; PID:q736090
##experimental_source isolate patient Ferracuti '83
#accession S53209
#molecule_type DNA
#residues 1-212 #label LA2
##cross-references EMBL:X85290; NID:q736114; PID:q736116
##experimental_source isolate patient Castag '83
#accession S53234
#molecule_type DNA
#residues 1-212 #label LA3
##cross-references EMBL:X85300; NID:q736150; PID:q736152
##experimental_source isolate patient Sanna '84
#accession S53264
#molecule_type DNA
#residues 1-212 #label LA4
##cross-references EMBL:X85313; NID:q736194; PID:q736196

```
##experimental_source isolate patient Licheri-1'85
#accession S53249
##molecule_type DNA
##residues 1-212 ##label LA5
##cross-references EMBL:X85306; NID:g736172; PID:g736174
##experimental_source isolate patient Flore-1'86
#accession S53262
##molecule_type DNA
##residues 1-212 ##label LA6
##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
#accession S53277
##molecule_type DNA
##residues 30-212 ##label LA7
##cross-references EMBL:X85317; NID:g736211; PID:g736214
##experimental_source patient Giordo-2'86
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be processed

REFERENCE A93214
#authors Galibert, F.; Mandart, E.; Fitoussi, F.; Tellois, P.;
#journal Charney, P.
#title Nature (1979) 281:646-650
#feature Nucleotide sequence of the hepatitis B virus genome (subtype
#accession A03711
#cross-references M01D:81012091
##molecule_type DNA
##residues 1-212 ##label GAL
##cross-references GB:J02203; NID:g329640; PID:g329642
##experimental_source subtype ayw

GENETICS
#gene C
#classification #superfamily hepatitis B virus core antigen
#keywords alternative initiators; core protein
FEATURE
1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP
SUMMARY #length 212 #molecular-weight 24350 #checksum 782

Query Match 76.6%; Score 1375; DB 1; Length 212;
Best Local Similarity 99.5%; Pred. No. 4.47e-198;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 88
:|||||
QY 57 SMDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 116
|||||
Db 89 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 148
|||||
QY 117 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 176
|||||
Db 149 VSGFWIRTPPAPRNAPILSTLPTTVVRRGRSPRRRPSRRRSOSPRRRSOSR 208
|||||
QY 177 VSGFWIRTPPAPRNAPILSTLPTTVVRRGRSPRRRPSRRRSOSPRRRSOSR 236
|||||
Db 209 ESOC 212
|
QY 237 ESOC 240

RESULT 2
ENTRY S53211 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Castag-1'85 and others)
ALTERNATE_NAMES HBC antigen; HBe antigen precursor / HBC antigen; pre-C/C
antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Castag-1'85; isolate patient Ferracuti-1'89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
```

```
08-Sep-1997
S53211; S53197
ACCESSIONS
REFERENCE
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53211
##molecule_type DNA
##residues 1-212 ##label LA1
##cross-references EMBL:X85291; NID:g736117; PID:g736119
##experimental_source isolate patient Castag-1'85
#accession S53197
##molecule_type DNA
##residues 30-212 ##label LAW
##cross-references EMBL:X85284; NID:g736095; PID:g736098
##experimental_source isolate patient Ferracuti-1'89
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
#classification #superfamily hepatitis B virus core antigen
#keywords alternative initiators; core protein
FEATURE
1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #product e antigen #status predicted #label EAG\
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP
SUMMARY #length 212 #molecular-weight 24336 #checksum 746

Query Match 76.5%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 6.55e-198;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 88
:|||||
QY 57 SMDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 116
|||||
Db 89 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 148
|||||
QY 117 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 176
|||||
Db 149 VSGFWIRTPPAPRNAPILSTLPTTVVRRGRSPRRRPSRRRSOSPRRRSOSR 208
|||||
QY 177 VSGFWIRTPPAPRNAPILSTLPTTVVRRGRSPRRRPSRRRSOSPRRRSOSR 236
|||||
Db 209 ESOC 212
|
QY 237 ESOC 240

RESULT 3
ENTRY S32204 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C1000)
ALTERNATE_NAMES HBe antigen precursor / HBC antigen; pre-C/C antigen
core antigen; e antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient C1000
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997
S32204
ACCESSIONS
REFERENCE S32202
#authors Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.;
Gerok, W.; Rasenack, J.
#submission submitted to the EMBL Data Library, March 1993
#description Identification and sequence analysis of hepatitis B virus DNA
in immunological negative infection.
#accession S32204
##molecule_type DNA
##residues 1-212 ##label PRE
##cross-references EMBL:X72702; NID:g286927; PID:g286930
##experimental_source subtype ayw, patient C1000
#note due to a stop codon between the alternative initiators
```

GENETICS the e antigen precursor cannot be produced

CLASSIFICATION C
#superfamily hepatitis B virus core antigen
KEYWORDS core protein
FEATURE 1-29

30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link ENG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24336 #checksum 770

Query Match 76.5%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 6.55e-198;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPVSVDLDTASALYRDALSPHCSPHHTALROAI 88
117 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRVTEYL 148
117 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRVTEYL 176

Db 149 VSGFWIRTPPAYRPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
177 VSGFWIRTPPAYRPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 236

Db 209 ESOC 212
237 ESOC 240

RESULT 4
ENTRY S53207 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Castaa-2'87)

ALTERNATE_NAMES HBC antigen
CONTAINS #formal_name hepatitis B virus, HBV
ORGANISM #isolate patient Castaa-2'87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53207
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission Submitted to the EMBL Data Library, March 1995
#accession S53207

#molecule_type DNA
#residues 1-183 #label LAI
#cross-references EMBL:X85289; NID:9736110; PID:9736113
#experimental_source Isolate patient Castaa-2'87
#note due to a stop codon between the alternative initiators the e antigen precursor cannot be produced

GENETICS C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
SUMMARY #length 183 #molecular-weight 21102 #checksum 2165

Query Match 76.4%; Score 1373; DB 2; Length 183;
Best Local Similarity 99.5%; Pred. No. 9.59e-198;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKFEGATVELLSFLPSDFPVSVDLDTASALYRDALSPHCSPHHTALROAI 60
58 MDIDPKFEGATVELLSFLPSDFPVSVDLDTASALYRDALSPHCSPHHTALROAI 117

Db 61 CMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRVTEYL 120
118 CMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRVTEYL 177

Db 121 SFGWIRTPPAYRPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSRE 180
178 SFGWIRTPPAYRPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSRE 237

Db 181 SOC 183
238 SOC 240

RESULT 5
ENTRY S20750 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus (subtype ayw, patient C1)

ALTERNATE_NAMES HBE antigen precursor / HBC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
DATE subtype ayw, patient C1
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS S20750
REFERENCE S20745
#authors Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.
#submission Submitted to the EMBL Data Library, March 1992
#description Sequence analysis of HBV genomes isolated from patients with HBsAg negative chronic liver disease.

#accession S20750
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X5258; NID:959434; PID:959436
#experimental_source subtype ayw, patient C1

GENETICS C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE 1-29

30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link ENG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 147

Query Match 76.4%; Score 1373; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 9.59e-198;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPVSVDLDTASALYRDALSPHCSPHHTALROAI 88
57 SMDIDPKFEGATVELLSFLPSDFPVSVDLDTASALYRDALSPHCSPHHTALROAI 116

Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRVTEYL 148
117 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRVTEYL 176

Db 149 VSGFWIRTPPAYRPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
177 VSGFWIRTPPAYRPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 236

Db 209 ESOC 212
237 ESOC 240

RESULT 6
ENTRY S53270 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Licheri-2'87)

ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Licheri-2'87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

```

ACCESSIONS      08-Sep-1997
REFERENCE       S533270
#authors       Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submition     Submitted to the EMBL Data Library, March 1995
#accession     S533270
#molecule_type DNA
#residues     1-183 #label LAI
##cross-references EMBL:X85314; NID:g736201; PID:g736204
##experimental_source isolate patient Licheri-2/87
#note          due to a stop codon between the alternative initiators
               the e antigen precursor cannot be produced

GENETICS
#gene          C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS       core protein
SUMMARY        #length 183 #molecular-weight 21102 #checksum 2199

Query Match    76.3%; Score 1370; DB 2; Length 183;
Best Local Similarity 98.4%; Pred. No. 3,01e-197;
Matches 180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Dd 1 MDIDPKFGATVELSLPSDFPFSVDLIDTASALYKDLSEPEHCSPHHTLRQAIL 60
    |||||
Qy 58 MDIDPKFGATVELSLPSDFPFSVDLIDTASALYKDLSEPEHCSPHHTLRQAIL 117
    |||||
Dd 61 CMGDLMTATWGVNLDEPASRDVLSVNTNMGLKFMHSCITFSEREVIETLY 120
    |||||
Qy 118 CMGELMTATWGVNLDEPASRDVLSVNTNMGLKFMHSCITFSEREVIETLY 177
    |||||
Dd 121 SFGVMIRTPAPYRPENADILSTPEITVRRRGRTPRRRPSPRRRSQSPRRRSQSRE 180
    |||||
Qy 178 SFGVMIRTPAPYRPENADILSTPEITVRRRGRTPRRRPSPRRRSQSPRRRSQSRE 237
    |||||
Dd 181 SQC 183
    ||||
Qy 238 SQC 240

RESULT 7
ENTRY   S53326 #type complete
TITLE   e antigen precursor / core antigen - hepatitis B virus
         (isolate patient Castag'3)
ALTERNATE_NAMES
CONTAINS HBe antigen precursor / HBe antigen; pre-C/C antigen
ORGANISM core antigen; e antigen
          #formal_name hepatitis B virus, HBV
          #isolate_patient Castag'3
          #variety 08-Jul-1995 #sequence_revision 03-Aug-1995 #text-change
          08-Sep-1997
ACCESSIONS S53326
REFERENCE  S53312
#authors  Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submition Submitted to the EMBL Data Library, March 1995
#accession S53326
#molecule_type DNA
#residues 1-212 #label LAI
##cross-references EMBL:X85293; NID:g736124; PID:g736126
##experimental_source isolate patient Castag'3

GENETICS
#gene          C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS       alternative initiators; core protein
SUMMARY        #length 212 #molecular-weight 24363 #checksum 752

Query Match    76.3%; Score 1370; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 3,01e-197;
Matches 182; Conservative 1; Indels 0; Gaps 0;

```

Db	29	GMDIDPYKEFGATVYELSLFSDSPFSVRDLDDNASALYREALSPESCSPHHTALROAI	88
Oy	57	SMDDIDPYKEFGATVYELSLFSDSPFSVRDLDDNASALYREALSPESCSPHHTALROAI	116
Db	89	LCWGLMNTLATWGVNLEDPAASRDLYSVYVNTNMGKFRQLMFWHISCLTFGRETIVIEL	148
Oy	117	LCWGLMNTLATWGVNLEDPAASRDLYSVYVNTNMGKFRQLMFWHISCLTFGRETIVIEL	176
Db	149	VSFQWITTPRAYRPNPAPILSTLPETTVVRRGRGSPRRRTPSPRRRSQSPRRRSQSR	208
Oy	177	VSFQWITTPRAYRPNPAPILSTLPETTVVRRGRGSPRRRTPSPRRRSQSPRRRSQSR	236
Db	209	ESOC 212	
Oy	237	ESOC 240	
RESULT	8		
ENTRY		S53272	#type complete
TITLE		e antigen precursor / core antigen - hepatitis B virus (isolate patient Lichner1-3/90)	
ALTERNATE_NAMES		HBe antigen precursor / HBeC antigen; pre-C/C antigen	
CONTAINS		core antigen; e antigen	
ORGANISM		#formal_name hepatitis B virus, HBV	
Variety		isolate patient Lichner1-3/90	
DATE		08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997	
ACCESSIONS		S53272	
REFERENCE		S53112	
#authors		LaI, M.E.; Mazzioleni, A.P.; Porru, A.; Balestrieri, A.	
#submission		submitted to the EMBL Data Library, March 1995	
#accession		S53272	
#molecule_type		DNA	
#residues		1-212 #label LAI	
#cross-references		EMBL:X85315; NID:g736205; PID:g736207	
GENETICS		#experimental_source isolate patient Lichner1-3/90	
#gene		C	
CLASSIFICATION		#superfamily hepatitis B virus core antigen	
KEYWORDS		alternative initiators; core protein	
FEATURE			
1-29		#domain signal sequence #status predicted #label SIG\	
30-212		#product core antigen #status predicted #label CAG\	
179-212		#product e antigen #status predicted #label EAG\	
		#domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP	
SUMMARY		#length 212 #molecular-weight 24366 #checksum 446	
Query Match		76.3%; Score 1370; DB 2; Length 212;	
Best Local Similarity		98.9%; Pred. No. 3,016-197;	
Matches 182; Conservative		1; Mismatches 1; Indels 0; Gaps 0	
Db	29	GMDIDPYKEFGATVYELSLFSDSPFSVRDLDDNASALYREALSPESCSPHHTALROAI	88
Oy	57	SMDDIDPYKEFGATVYELSLFSDSPFSVRDLDDNASALYREALSPESCSPHHTALROAI	116
Db	89	LCWGLMNTLATWGVNLEDPAASRDLYSVYVNTNMGKFRQLMFWHISCLTFGRETIVIEL	148
Oy	117	LCWGLMNTLATWGVNLEDPAASRDLYSVYVNTNMGKFRQLMFWHISCLTFGRETIVIEL	176
Db	149	VSFQWITTPRAYRPNPAPILSTLPETTVVRRGRGSPRRRTPSPRRRSQSPRRRSQSR	208
Oy	177	VSFQWITTPRAYRPNPAPILSTLPETTVVRRGRGSPRRRTPSPRRRSQSPRRRSQSR	236
Db	209	ESOC 212	
Oy	237	ESOC 240	
RESULT	9		
ENTRY		S53163	#type complete
TITLE		e antigen precursor / core antigen - hepatitis B virus	

ALTERNATE_NAMES (isolate patient Vitorina '92)
CONTAINS HBe antigen precursor / Hbc antigen: pre-C/C antigen
ORGANISM core antigen; e antigen
#formal_name hepatitis B virus, HBV
#variety isolate patient Vitorina '92
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53163
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53163
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85256; NID:9736050; PID:9736052
#experimental_source isolate patient Vitorina '92

GENETICS C
#gene #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE 1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product e antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24322 #checksum 842

Query Match 76.2%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 4,40e-197;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||
Oy 57 SMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 116
|||
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIISCLTFGRETIVLYL 148
|||||
Oy 117 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIISCLTFGRETIVLYL 176
|||||
Db 149 VSGFWITPPAYRPPNPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
|||||
Oy 177 VSGFWITPPAYRPPNPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 236
|||||

Db 209 ESOC 212
Oy 237 ESOC 240

RESULT 10
ENTRY S20746 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen: pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety subtype ayw, patient C
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS S20746
REFERENCE S20745
#authors Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
#submission submitted to the EMBL Data Library, March 1992
#description Sequence analysis of HBV genomes isolated from patients with HBeAg negative chronic liver disease.
#accession S20746
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X65257; NID:959429; PID:959431
#experimental_source subtype ayw, patient C

GENETICS C
#gene

CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE 1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product e antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 506

Query Match 76.2%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 4,40e-197;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||
Oy 57 SMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 116
|||
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIISCLTFGRETIVLYL 148
|||||
Oy 117 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIISCLTFGRETIVLYL 176
|||||
Db 149 VSGFWITPPAYRPPNPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
|||||
Oy 177 VSGFWITPPAYRPPNPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 236
|||||

Db 209 ESOC 212
Oy 237 ESOC 240

RESULT 11
ENTRY S53225 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Chighine-2/86)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen: pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Chighine-2/86
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53225
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53225
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85296; NID:9736137; PID:9736139
#experimental_source isolate patient Chighine-2/86

GENETICS C
#gene
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE 1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product e antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24308 #checksum 655

Query Match 76.2%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 4,40e-197;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||
Oy 57 SMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 116
|||
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIISCLTFGRETIVLYL 148
|||||
Oy 117 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFIISCLTFGRETIVLYL 176
|||||

Db 149 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRGSRPRRRRSQSPRRRRSQSR 208
117 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRGSRPRRRRSQSPRRRRSQSR 236
QY 209 ESOC 212
117
QY 237 ESOC 240

RESULT 12
ENTRY S53198 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Ferracuti-2/90)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen: pre-C/C antigen
CONTAINS core antigen: e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Ferracuti-2/90
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53198
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53198
#molecule_type DNA
#residues 1-212 ##label LAI
##cross-references EMBL:X85285; NID:q736099; PID:q736100
##experimental_source isolate patient Ferracuti-2/90

GENETICS C
#gene #superfamily hepatitis B virus core antigen
CLASSIFICATION #alternative initiators: core protein
KEYWORDS
FEATURE 1-29
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24292 #checksum 593

Query Match 76.2%; Score 1368; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 6,45e-197;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 88
57 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 116
QY 89 LCGDMLSLATWGVNLEDPASRDVLSVYNTNMGKLFROLMEHISCLTFGRTVIEYL 148
117 LCGELMTLATWGVNLEDPASRDVLSVYNTNMGKLFROLMEHISCLTFGRTVIEYL 176
Db 149 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRGSRPRRRRSQSPRRRRSQSR 208
117 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRGSRPRRRRSQSPRRRRSQSR 236
QY 209 ESOC 212
117
QY 237 ESOC 240

RESULT 13
ENTRY S53223 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Chigline-1/85)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen: pre-C/C antigen
CONTAINS core antigen: e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Chigline-1/85
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53223

REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53223
#molecule_type DNA
#residues 1-212 ##label LAI
##cross-references EMBL:X85295; NID:q736134; PID:q736136
##experimental_source isolate patient Chigline-1/85

GENETICS C
#gene #superfamily hepatitis B virus core antigen
CLASSIFICATION #alternative initiators: core protein
KEYWORDS
FEATURE 1-29
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24364 #checksum 1123

Query Match 76.1%; Score 1366; DB 2; Length 212;
Best Local Similarity 97.8%; Pred. No. 1.38e-196;
Matches 180; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 88
57 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 116
QY 89 LCGDMLSLATWGVNLEDPISRDVLSVYNTNMGKLFROLMEHISCLTFGRTVIEYL 148
117 LCGELMTLATWGVNLEDPASRDVLSVYNTNMGKLFROLMEHISCLTFGRTVIEYL 176
Db 149 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRGSRPRRRRSQSPRRRRSQSR 208
117 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRGSRPRRRRSQSPRRRRSQSR 236
QY 209 ESOC 212
117
QY 237 ESOC 240

RESULT 14
ENTRY S53274 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Giordo/84)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen: pre-C/C antigen
CONTAINS core antigen: e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Giordo/84
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53274
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53274
#molecule_type DNA
#residues 1-212 ##label LAI
##cross-references EMBL:X85316; NID:q736208; PID:q736210
##experimental_source isolate patient Giordo/84

GENETICS C
#gene #superfamily hepatitis B virus core antigen
CLASSIFICATION #alternative initiators: core protein
KEYWORDS
FEATURE 1-29
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24376 #checksum 390

Query Match 76.1%; Score 1366; DB 2; Length 212;

Best Local Similarity 98.9%; Pred. No. 1.38e-196;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVLLSLPDSDFPSVRLDITASALYREALSEPHCSPHHTALROAI 88
:|||||
Qy 57 SMDIDPYKEFGATVLLSLPDSDFPSVRLDITASALYREALSEPHCSPHHTALROAI 116
:|||||
Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 148
:|||||
Qy 117 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 176
:|||||
Db 149 VSEGVWIRTPPARPPNAPILSLPETVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 208
:|||||
Qy 177 VSEGVWIRTPPARPPNAPILSLPETVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 236
:|||||
Db 209 ESOC 212
:|||||
Qy 237 ESOC 240

RESULT 15
ENTRY S53169 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Muresu'89)
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Muresu'89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS
REFERENCE S53169
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53169
##molecule_type DNA
##residues 1-183 ##label LAI
##cross-references EMBL:X85275; NID:g736057; PID:g736060
##experimental_source isolate patient Muresu'89
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
SUMMARY #length 183 #molecular-weight 21088 #checksum 1849

Query Match 75.9%; Score 1364; DB 2: Length 183;
Best Local Similarity 98.4%; Pred. No. 2.96e-196;
Matches 180; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDIDPYKEFGATVLLSLPDSDFPSVRLDITASALYREALSEPHCSPHHTALROAI 60
:|||||
Qy 58 MDIDPYKEFGATVLLSLPDSDFPSVRLDITASALYREALSEPHCSPHHTALROAI 117
:|||||
Db 61 CWMELMTLATWGVNLEDPASRDVSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 120
:|||||
Qy 118 CWMELMTLATWGVNLEDPASRDVSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 177
:|||||
Db 121 SFGVWIRTPPARPPNAPILSLPETVVRRRGRTPRRRTSPRRRSQSPRRRSQSR 180
:|||||
Qy 178 SFGVWIRTPPARPPNAPILSLPETVVRRRGRTPRRRTSPRRRSQSPRRRSQSR 237
:|||||
Db 181 SOC 183
:|||||
Qy 238 SOC 240

Search completed: Thu Dec 16 13:13:06 1999
Job time : 72 secs.

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db 1 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 60
OY 58 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 117
Db 61 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFKROLMFHISCLTFGREYEV 120
OY 118 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFKROLMFHISCLTFGREYEV 177
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRPTSPRRRSOSRRRSOSRE 180
OY 178 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRPTSPRRRSOSRRRSOSRE 237
Db 181 SOC 183
OY 238 SOC 240
```

RESULT 2
ID CORA_HPEV2 STANDARD: PRT: 211 AA.

AC P24023;
DT 01-MAR-1992 (REL. 21, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DE CORE ANTIGEN.

GN C.
OS HEPATITIS B VIRUS (STRAIN ALPHA1).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE: 90266476.
RA TONG S., LI J., VITVITSKI L., TREPO C.;

RT "Active hepatitis B virus replication in the presence of anti-Hbe is associated with viral variants containing an inactive pre-C region.";
RL VIROLOGY 176:596-603(1990).

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CC or send an email to license@isb-sib.ch).

CC EMBL: M32138; G495034; ALT_SEQ.
DR PIR: A34773; NKVL1.

DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT

FT REPEAT 183 190
FT REPEAT 198 206

SO SEQUENCE 211 AA; 24208 MW; 0924CE5E CRC32;

Query Match 75.64; Score 1358; DB 1; Length 211;
Best Local Similarity 95.28; Pred. No. 2.15e-223;

Matches 179; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Db 24 LGWLMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 83
OY 53 LGWLMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 112
```

```
Db 84 ROAILCWDGLITLSTWGVNLEDPASRDLYSVYNTNMGKLFKROLMFHISCLTFGREYEV 143
OY 113 ROAILCWDGLITLSTWGVNLEDPASRDLYSVYNTNMGKLFKROLMFHISCLTFGREYEV 172
```

```
Db 144 IEVLVSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRPTSPRRRSOSRRRS 203
OY 173 IEVLVSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRPTSPRRRSOSRRRS 232
```

```
Db 204 TOSRESOC 211
OY 233 SOSRESOC 240
```

RESULT 3
ID CORA_HPEV2 STANDARD: PRT: 183 AA.

AC P03147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)

DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADYW).

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE: 81012115.
RA PASER M., GOTO T., GILBERT W., ZINK B., SCHALLER H., MCKAY P.,

RT "Hepatitis B virus genes and their expression in E. coli.";
RL NATURE 282:575-579(1979).

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CC or send an email to license@isb-sib.ch).

CC EMBL: J02202; G329638; -;
DR EMBL: A08967; G411874; -;

DR PIR: B93217; NKVL2.
DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN; REPEAT
FT REPEAT 162 169
FT REPEAT 170 177

SO SEQUENCE 183 AA; 21042 MW; 6EA6B674 CRC32;

Query Match 75.18; Score 1349; DB 1; Length 183;
Best Local Similarity 96.78; Pred. No. 1.09e-221;

Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```
Db 1 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 60
OY 58 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 117
```

```
Db 61 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFKROLMFHISCLTFGREYEV 120
OY 118 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFKROLMFHISCLTFGREYEV 177
```

```
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRPTSPRRRSOSRRRSOSRE 180
OY 178 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRPTSPRRRSOSRRRSOSRE 237
```

```
Db 181 SOC 183
OY 238 SOC 240
```

RESULT 4
ID CORA_HPEV2 STANDARD: PRT: 183 AA.

AC P17392;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)

DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN OKIYAMA/P0DW282).

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RP SEQUENCE FROM N.A.

RA MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,

RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes.";

```

RL J. GEN.VIROL. 69:2575-2583(1988).
CC -----
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CC -----
DR EMBL: D00330; ; NOT_ANNOTATED_CDS.
DR PIR: B28925; NKVLJ2.
DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 115BDPE3 CRC32;

Query Match          74.4%; Score 1336; DB 1; Length 183;
Best Local Similarity 96.2%; Pred. No. 3,14e-219;
Matches 176; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db      1 MDIDYKEFGASVELSTFLSPDFPFSVDLDLTASATLYREALSEPHKSPHHTALROAIL 60
Qy      58 MDIDYKEFGATVLLSTLPSPDFPSVDLDLTASALTREALSEPKSPHHTALROAIL 117
Qy      61 CWGELMNLATWGVSNLEDPASRELVSYVNVMGKIRQLLMFHISCLTFGRETVLEYLV 120
Db      118 CWGELMTLATWGVNLEDPASRDLYSVYNTMGKLFQLLMFHSICLTFGRETVIEYL 177
Db      121 SFGVWRTPPAYRPPNAILSTLPETTYVRRGRSPRRRTPSPRRRRSOSPRRRRSORE 180
Qy      178 SFGVWRTPPAYRPPNAPILSTLPETTYVRRGRSPRRRTPSPRRRRSOSPRRRRSORE 237
Db      181 SOC 183
Qy      238 SOC 240

RESULT      5 STANDARD: PRF: 183 AA.
AC P03150; P03151;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADP), HEPATITIS B VIRUS (SUBTYPE ADRA4),
OS AND HEPATITIS B VIRUS (SUBTYPE ADM / STRAIN INDONESIA/PIDM420).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
CC (1)
RN RP SEQUENCE FROM N.A.
RC STRAIN-ADR:
RX MEDLINE: 83168919.
RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RL DNA: subtype adr and adw."
RN RP NUCLEIC ACIDS RES. 11:1747-1757(1983).
RC (2)
RN RP SEQUENCE FROM N.A.
RC STRAIN-ADR4;
RX MEDLINE: 83246570.
RA FUDUYAMA A., MIYANOHARA A., NOZANI C., YONEYAMA T., OHTOMO N.,
RT MATSUBARA K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RL adr."
RN RP NUCLEIC ACIDS RES. 11:4601-4610(1983).
RC (3)
RN RP SEQUENCE FROM N.A.
RC STRAIN-ADM;
RX OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSOMWONGJO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
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RT "Typing hepatitis B virus by homology in nucleotide sequence:"
RT Comparison of surface antigen subtyles.";
RL J. GEN. VIROL. 69:2575-2583(1988).
CC -----
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CC -----
DR EMBL; V00867; -- NOT_ANNOTATED_CDS.
DR EMBL; X01587; G59407; -- NOT_ANNOTATED_CDS.
DR PIR; A93480; NKVLAS.
DR PIR; B93460; NKYLAA.
DR PIR; C28925; NKYLJ3.
DR PFAM; PF00906; Hepatitis_core.1.
KM CORE PROTEIN; REPEAT.
FT REPEAT 162
FT REPEAT 169
FT FT 170
FT FT 177
SO SEQUENCE 183 AA; 21095 MW; DZELISB9 CRC32;

Query Match 74.3%; Score 1334; DB 1; Length 183;
Best Local Similarity 95.6%; Pred. No. 7,52e-219;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 MDIDYKEFGASVLESLPSDFPFISRDLDLTATGALYREALSPDHCPHTALQAIL 60
Oy 58 MDIDYKEFGATVELSLPSDFFSVDLDTATGALYREALSEPHKSPHTALQAIL 117
Db 61 CWGELMLNATWGSNLDEDPASRELVSYYNNMGKIRQLLMFHISCLTFGRETVLEYLY 120
Oy 118 CWGELMTLATWGVNLDEPDASRDLYSVYNTNMGLKFQLLMFHSICLTFGRETVLEYLY 177
Db 121 SFGWIKRPAYRRPNAILSTLPETTYVRRGRSPRRRTPSPRRRSOSPPRRRSOSQE 180
Oy 178 SFGWIKRPAYRRPNAILSTLPETTYVRRGRSPRRRTPSPRRRSOSPPRRRSOSQE 237
Db 181 SOC 183
Oy 238 SOC 240

RESULT 6 STANDARD; PRT; 183 AA.
AC CORA.HPBVJ
ID P17391.
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN JAPAN/PJDM2233).
OC VIRUSES; RETROID VIRUSES; HERPANA VIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RX MEDLINE; 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASUROSEMIUNJO R.I., IMAI M.,
RA MIYAKAWA Y., MATSUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:"
RT Comparison of surface antigen subtyles.";
RL J. GEN. VIROL. 69:2575-2583(1988).
RC -----
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CC -----
DR EMBL; D00329; -- NOT_ANNOTATED_CDS.
DR PIR; A28925; NKVLJ1.
```

DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA: 21224 MW: F6B348B6 CRC32:

Query Match 73.6%; Score 1322; DB 1; Length 183;
Best local Similarity 96.2%; Pred. No. 1,40e-216;
Matches 176; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 MDIDPKKEGATVLLSLPDSFPSSRDLDTPASALYREALSPHCSPHHTALROAIL 60
QY 58 MDIDPKKEGATVLLSLPDSFPSSRDLDTPASALYREALSPHCSPHHTALROAIL 117
Db 61 CMGELMTLATVGNLDPASRDLYVYVNTNMGKIRQLMFIISCLTGTGRETVELEY 120
QY 118 CMGELMTLATVGNLDPASRDLYVYVNTNMGKIRQLMFIISCLTGTGRETVELEY 177
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQ 180
QY 178 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQ 237
Db 181 SOC 183
QY 238 SOC 240

RESULT 7
ID CORA_HPBVT STANDARD: PRT: 185 AA.

AC P03149;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.

OS HEPATITIS B VIRUS (SUBTYPE ADW)
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN 11)
RP SEQUENCE FROM N.A.

RX MEDLINE: 83168919.

RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;

RT "The complete nucleotide sequences of the cloned hepatitis B virus

DNA; subtype adr and adw.";

RL NUCLEIC ACIDS RES. 11:1747-1757(1983).

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CC EMBL: V00866; NOT_ANNOTATED_CDS.

DR PIR: C93460; NKVLA6.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN; REPEAT.

FT REPEAT 164 171

FT REPEAT 172 179

SQ SEQUENCE 185 AA: 21394 MW: 791E0381 CRC32:

Query Match 73.6%; Score 1321; DB 1; Length 185;

Best local Similarity 96.2%; Pred. No. 2.17e-216;
Matches 178; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Db 1 MDIDPKKEGATVLLSLPDSFPSSRDLDTPASALYREALSPHCSPHHTALROAIL 60
QY 58 MDIDPKKEGATVLLSLPDSFPSSRDLDTPASALYREALSPHCSPHHTALROAIL 117
Db 61 CMGELMTLATVGNLDPASRDLYVYVNTNMGKIRQLMFIISCLTGTGRETVELEY 120
QY 118 CMGELMTLATVGNLDPASRDLYVYVNTNMGKIRQLMFIISCLTGTGRETVELEY 177

Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQ 180
QY 178 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQ 235
Db 181 RESOC 185
QY 236 RESOC 240

RESULT 8

ID CORA_HPBVT STANDARD: PRT: 195 AA.

AC P29178;

DT 01-DEC-1992 (REL. 24, CREATED)

DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)

DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

OS HEPATITIS B VIRUS (SUBTYPE ADW2 VARIANT SF)

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN 11)
RP SEQUENCE FROM N.A.

RX MEDLINE: 90169850.

RA BHAT R.A., ULRICH P.P., VYAS G.N.;

RT "Molecular characterization of a new variant of hepatitis B virus in

a persistently infected homosexual man.";

RL HEPATOLOGY 11:271-276(1990).

DR PIR: A37182; NKVLA3.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN; REPEAT.

FT REPEAT 174 181

FT REPEAT 182 189

SQ SEQUENCE 195 AA: 22461 MW: AF3DB5F3 CRC32:

Query Match 73.2%; Score 1314; DB 1; Length 195;

Best local Similarity 93.5%; Pred. No. 4.57e-215;
Matches 173; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 11 FGIDIDPKKEGATVLLSLPDSFPSSRDLDTPASALYREALSPHCSPHHTALROA 70

QY 56 LSMDIDPKKEGATVLLSLPDSFPSSRDLDTPASALYREALSPHCSPHHTALROA 115

Db 71 ILGWELMTLATVGNLDPASRDLYVYVNTNMGKIRQLMFIISCLTGTGRETVELEY 130

QY 116 ILGWELMTLATVGNLDPASRDLYVYVNTNMGKIRQLMFIISCLTGTGRETVELEY 175

Db 131 LVSEGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQ 190

QY 176 LVSEGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTPSPRRRSQSPRRRSQ 235

Db 191 RESOC 195

QY 236 RESOC 240

RESULT 9

ID CORA_HPBVT STANDARD: PRT: 212 AA.

AC Q05495;

DT 01-NOV-1995 (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

OS HEPATITIS B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE W4B).

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN 11)
RP SEQUENCE FROM N.A.

RX MEDLINE: 93346970.

RA NAUMANN H., SCHAEFER S., YOSHIDA C.F.T., GASPAR A.M.C., REPP R.,

RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil

that expresses HBV surface antigen subtype adw4.";

RL J. GEN. VIROL. 74:1627-1632(1993).

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DR EMBL: X69798; G59423; -

DR PFAM: PF00906; Hepatitis_core: 1.

KW CORE PROTEIN: REPEAT 1.

FT DOMAIN 178 204 ARG-RICH.

FT REPEAT 184 203 3 X 5 AA REPEATS OF S-P-R-R-R.

FT REPEAT 184 188 1.

FT REPEAT 191 195 2.

FT REPEAT 199 203 3.

SO SEQUENCE 212 AA; 24234 MW; BCCDF263 CRC32;

Query Match 73.1%; Score 1313; DB 1; Length 212;
Best Local Similarity 92.9%; Pred. No. 7,06e-215;
Matches 171; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

DB 29 GMDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAIL 88
QY 57 SMDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAIL 116
DB 89 LCMGELMTLASVGNLLEDPASRDVSVVNTNMGLKIRQLLMFHSCLTFGRVLEYL 148
QY 117 LCMGELMTLASVGNLLEDPASRDVSVVNTNMGLKIRQLLMFHSCLTFGRVLEYL 176
DB 149 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSP 208
QY 177 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSP 236
DB 209 ASOC 212
QY 237 ESOC 240

RESULT 10
ID CORA_HPBVL STANDARD; PRT: 183 AA.

AC P12901;

DT 01-OCT-1989 (REL. 12, CREATED)

DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)

DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

GN C.

OS HEPATITIS B VIRUS (STRAIN LSH / CHIMPANZEE ISOLATE).

CC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 88258473.

RA VAUDIN M., WOLSTENHOLME A.J., TSIOUAVE K.N., ZUCKERMAN A.J.,

RT HARRISON T.J.;

RT "The complete nucleotide sequence of the genome of a hepatitis B

RT virus isolated from a naturally infected chimpanzee";

RL J. GEN. VIROL. 69:1383-1389(1988).

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DR EMBL: D00220; D100603; -

DR PIR: A28885; NKVLCF.

DR PFAM: PF00906; Hepatitis_core: 1.

KW CORE PROTEIN: REPEAT.

FT REPEAT 162 169

FT REPEAT 170 177

SO SEQUENCE 183 AA; 20999 MW; 1AF57C9 CRC32;

Query Match 72.8%; Score 1308; DB 1; Length 183;
Best Local Similarity 94.5%; Pred. No. 6.23e-214;
Matches 173; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAIL 60

QY 58 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAIL 117

DB 61 CWMGELMTLASVGNLLEDPASRDVSVVNTNMGLKIRQLLMFHSCLTFGRVLEYL 120

QY 118 CWMGELMTLASVGNLLEDPASRDVSVVNTNMGLKIRQLLMFHSCLTFGRVLEYL 177

DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSPA 180

QY 178 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSPRE 237

DB 181 SOC 183

QY 238 SOC 240

RESULT 11
ID CORA_HPBV2 STANDARD; PRT: 185 AA.

AC P03148;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

GN C.

OS HEPATITIS B VIRUS (SUBTYPE ADW2).

CC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]

RP SEQUENCE FROM N.A.

RA VALENZUELA P., QUIROGA M., ZALDIVAR J., GRAY P., RUTTER W.J.;

RL (IN) FIELD B.N., JAENISCH R., FOX C.F. (EDS.);

RL ANIMAL VIRUS GENETICS, PP. 57-70, ACADEMIC PRESS, NEW YORK (1980).

DR PIR: A94409; NKVLA3.

DR PFAM: PF00906; Hepatitis_core: 1.

KW CORE PROTEIN: REPEAT.

FT REPEAT 164 171

FT REPEAT 172 179

SO SEQUENCE 185 AA; 21304 MW; E2EA3360 CRC32;

Query Match 72.7%; Score 1305; DB 1; Length 185;
Best Local Similarity 95.7%; Pred. No. 2.30e-213;
Matches 177; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

DB 1 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAIL 60

QY 58 MDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALROAIL 117

DB 61 CWMGELMTLASVGNLLEDPASRDVSVVNTNMGLKIRQLLMFHSCLTFGRVLEYL 120

QY 118 CWMGELMTLASVGNLLEDPASRDVSVVNTNMGLKIRQLLMFHSCLTFGRVLEYL 177

DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSP 180

QY 178 SFGVWIRTPPAYRPPNAPILSTLPETTVVRR--GRSPRRRTPSPRRRSQSPRRRSQSP 235

DB 181 RESOC 185

QY 236 RESOC 240

RESULT 12
ID CORA_HPBV9 STANDARD; PRT: 214 AA.

AC P17099;

DT 01-AUG-1990 (REL. 15, CREATED)

DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)

DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

GN C.

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OS HEPATITIS B VIRUS (SUBTYPE ADM / STRAIN 991).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RA SEQUENCE FROM N.A.
RP KOECHL H.G., SCHUELER A., LOTTMANN S., THOMSEN R.;
RL SUBMITTED (FEB-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
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CC -----
DR EMBL: X51970; G60433; -.
DR PIR: S10381; NKVLK5.
DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 786CD048 CRC32;

Query Match 72.6%; Score 1304; DB 1; Length 214;
Best Local Similarity 95.2%; Pred. No. 3,56e-213;
Matches 177; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Db 29 GMDIDPKKFGATVELLSFLPSDFPSVRDLDTASLVRALAESEPHSHHTALROI 88
:|||||
Qy 57 SMDIDPKKFGATVELLSFLPSDFPSVRDLDTASLVRALAESEPHSHHTALROI 116
:|||||

Db 89 LCMGELMTLATWVGNNEDEPASRDLYVNVYNTMGKIRQLMFRISYLTFGRETVLEYL 148
|||||
Qy 117 LCMGELMTLATWVGNNEDEPASRDLYVNVYNTMGKIRQLMFRISYLTFGRETVLEYL 176
|||||

Db 149 VSFQVWIRTPPYAPPPNAPILSTLPETTVVRRDRGSPRRRTSPRRRSQSPRRRSQ 208
|||||
Qy 177 VSFQVWIRTPPYAPPPNAPILSTLPETTVVRRR--GRSPRRRTSPRRRSQSPRRRSQ 234
|||||

Db 209 SRESQC 214
|||||
Qy 235 SRESQC 240
|||||

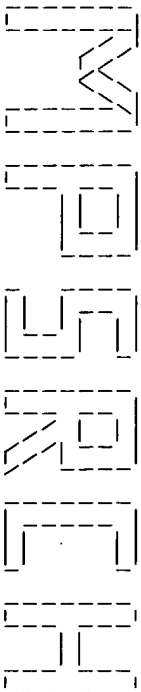
RESULT 13
ID CORA.MHV1 STANDARD; PRT; 188 AA.
AC P03152;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 1 (MHV 1),
OS WOODCHUCK HEPATITIS VIRUS 7 (MHV 7),
OS WOODCHUCK HEPATITIS VIRUS 59 (MHV 59), AND
OS WOODCHUCK HEPATITIS VIRUS 8 (INJECTION CLONE) (MHV 8).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RA SEQUENCE FROM N.A.
RP SPECIES=WOODCHUCK HEPATITIS VIRUS 1;
RX MEDLINE: 82216969.
RA GALIBERT F., CHEN T.N., MANDART E.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT comparison with the hepatitis B virus sequence.";
RL J. VIROL. 41:51-65(1982).
RN [2]
RA SEQUENCE FROM N.A.
RP SPECIES=WOODCHUCK HEPATITIS VIRUS 7, AND WOODCHUCK HEPATITIS VIRUS 59;
RX MEDLINE: 88101359.
RA COHEN J.I., MILLER R.H., ROSENBLUM B., DENNISTON K., GERIN J.L.,
RA PURCELL R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RT shows conservation of the genome.";

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RL VIRIOLOGY 162:12-20(1988).
[3]
RN SEQUENCE FROM N.A.
RP SPECIES=WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE);
RX MEDLINE; 89184524.
RA GIRONEL R., COTE P.J., HORNBuckle W.E., TENNANT B.C., GERIN J.L.,
RA PURELL R.H., MILLER R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
hepatitis virus that is infectious in the natural host";
RU PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
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DR EMBL; J02442; G336129; -
DR EMBL; M18752; G336140; -
DR EMBL; M19183; G336145; -
DR EMBL; J04514; G336149; -
DR PIR; A03713; NKVLC.
DR PIR; C32397; NKVLCT.
DR PIR; C32397; NKVLC4.
DR PIR; C32397; NKVLC3.
DR PFAM; PF00906; Hepatitis_core; 1.
KM CORE PROTEIN; REPEAT.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MM; A667DB27 CRC32;
Query Match 52.2%; Score 938; DB 1; Length 188;
Best Local Similarity 67.0%; Pred. No. 2 07e-144;
Matches 126; Conservative 25; Mismatches 32; Indels 5; Gaps 1;
Db 1 MDIDYKEFGSSYLNFPLDFPFDDNALVDYATALYEELTGREHSPPHHTAQLQALV 60
Qy 58 MDIDYKEGAGVELLSFLPSDFSVNDLDLTASALTREALSESHSPHTARQAAIL 117
    ||| | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 CWDELTKLIAMSSVITSEQVFTIIVNHVNDTWGLKVRQSILMFSLCTFGCHTYOEFV 120
    ||| | : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 118 CGEIMLTATATWGVNLDEPDASRDLYVSYSVTMTGMKLFQOLMFIHSCTFGRETYIEVLV 177
    ||| | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 SGGWTRPAPRPPNPAPTSLPEHTYIRRGARGASPRRRPSPRRRSOSPRRRR 180
Qy 178 SGGWTRPAPRPPNPAPTSLPETTVARRRG-----RSPRRRIPSPRRRSOSPRRRR 232
Db 181 SOSPSANC 188
    ||| : |
Qy 233 SOSRESQC 240
-----
RESULT 14 CORA_HPBGS STANDARD; PRF; 217 AA.
AC P03153;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS GROUND SQUIRREL HEPATITIS VIRUS (GSHV).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84267998.
RA SEBERG C., GANEM D., YARMUS H.E.;
RT "Nucleotide sequence of an infectious molecularly cloned genome of
ground squirrel hepatitis virus.";
RU J. VIROL. 51:367-375(1984).
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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 13:14:23 1999; Maspar time 17.75 Seconds
Tabular output not generated.

Title: >US3835-10-38183
Description: (1-240) from US3835-10-38183.pep
Perfect Score: 1796
Sequence: 1 MDIPYKEFGATVELLSFLP.....RRRSQSPRRRRSQSRESQC 240

Scoring table:
PAM 150
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl9
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 46.641; Variance 107.390; scale 0.434

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1375	76.6	212 14	089656	PRE-C/CORE.	9.01e-219
2	1374	76.5	212 14	068020	PRE-C/CORE.	1.37e-218
3	1374	76.5	212 14	089597	HBCAG.	1.37e-218
4	1373	76.4	183 14	089437	X, PREC AND C GENES (C	2.09e-218
5	1373	76.4	183 14	068008	X, PREC AND C GENES (F	2.09e-218
6	1373	76.4	212 14	067876	PRE C/C ORF.	2.09e-218
7	1372	76.4	212 14	011884	CORE ANTIGEN PRECURSOR	3.18e-218
8	1370	76.3	183 14	068066	X, PREC AND C GENES (L	7.37e-218
9	1370	76.3	212 14	068068	PRE-C/CORE.	7.37e-218
10	1370	76.3	212 14	068025	PRE-C/CORE.	7.37e-218
11	1369	76.2	212 14	067872	PRE C/C ORF.	1.12e-217
12	1369	76.2	212 14	067984	PRE-C/CORE.	1.12e-217
13	1369	76.2	212 14	068032	PRE-C/CORE.	1.12e-217
14	1368	76.2	212 14	068010	PRE-C/CORE.	1.12e-217
15	1366	76.1	212 14	068070	PRE-C/CORE.	3.96e-217
16	1366	76.1	212 14	068030	PRE-C/CORE.	3.96e-217
17	1364	75.9	183 14	067989	X, PREC AND C GENES (M	9.17e-217
18	1363	75.9	183 14	068048	X, PREC AND C GENES (F	1.40e-216
19	1363	75.9	212 14	068014	PRE-C/CORE.	1.40e-216
20	1363	75.9	212 14	068012	PRE-C/CORE.	1.40e-216

21	1363	75.9	212 14	067980	PRE-C/CORE.	1.40e-216
22	1362	75.8	212 14	068051	PRE-C/CORE.	2.13e-216
23	1360	75.7	212 14	089446	PRE-C/CORE.	4.92e-216
24	1360	75.7	212 14	068016	PRE-C/CORE.	4.92e-216
25	1360	75.7	212 14	096845	COMPLETE GENOME.	4.92e-216
26	1359	75.7	212 14	068053	PRE-C/CORE.	7.50e-216
27	1357	75.6	212 14	068075	PRE-C/CORE.	1.74e-215
28	1357	75.6	212 14	068077	PRE-C/CORE.	1.74e-215
29	1355	75.4	212 14	068045	PRE-C/CORE.	4.02e-215
30	1352	75.3	183 14	089531	CORE PROTEIN.	1.42e-214
31	1351	75.2	183 14	067946	C ANTIGEN.	2.16e-214
32	1351	75.2	212 14	089719	PRE-C/CORE.	2.16e-214
33	1349	75.1	183 14	067997	X, PREC AND C GENES (B	5.01e-214
34	1348	75.1	183 14	068037	X, PREC AND C GENES (D	7.62e-214
35	1348	75.1	183 14	068060	X, PREC AND C GENES (M	7.62e-214
36	1347	75.0	212 14	067912	PRE-CORE/CORE PROTEIN	1.16e-213
37	1345	74.9	183 14	067973	X, PREC AND C GENES (T	2.69e-213
38	1343	74.8	183 14	068023	X, PREC AND C GENES (C	6.12e-213
39	1344	74.8	212 14	092918	PRE-C/CORE.	4.09e-213
40	1344	74.8	212 14	068035	PRE-C/CORE.	4.09e-213
41	1342	74.7	183 14	067964	X, PREC AND C GENES (F	9.47e-213
42	1341	74.7	183 14	068064	X, PREC AND C GENES (S	1.44e-212
43	1341	74.7	183 14	068003	X, PREC AND C GENES (S	1.44e-212
44	1341	74.7	212 14	068042	PRE-C/CORE.	1.44e-212
45	1341	74.7	212 14	081115	HBEAG,HBCAG.	1.44e-212

ALIGNMENTS

RESULT	ID	1	PRELIMINARY;	PRT;	212 AA.
AC	089656;				
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)				
DE	PRE-C/CORE.				
GN	HEPATITIS B VIRUS.				
OS	HEPATITIS B VIRUS.				
OC	VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-PATIENT LICHERI-1'85.				
RA	LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;				
RL	SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-AYWA.				
RA	PLUCIENNICZAK A.;				
RL	SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 81012091.				
RA	GALLIBERT F., MANDART E., FINOUSSI F., TIOLLAIS P., CHANAY P.;				
RT	"Nucleotide sequence of the hepatitis B virus genome (subtype ayw)				
RT	cloned in E. coli."				
RL	NATURE 281:646-650(1979).				
RL	[4]				
RP	SEQUENCE FROM N.A.				
RA	BORISOVA G.P., POMPEN P.P., BYCHKO V.V., PUSHKO P.M., KALIS Y.V.,				
RA	DISHLER A.V., GREN E.Y., TSIBINOGIN V.V., KUKAIN R.A.;				
RL	DOKL. BIOCHEM. 279:386-390(1985).				
DR	EMBL: X85290; G736116; -				
DR	EMBL: X85300; G736152; -				
DR	EMBL: X85313; G736196; -				
DR	EMBL: X85283; G736090; -				
DR	EMBL: X85306; G736174; -				
DR	EMBL: X85316; G527437; -				
DR	EMBL: J02203; G329642; -				
DR	EMBL: X85312; G736193; -				
DR	PFAM: PF00906; HepatitisS_core; 1.				
KW	SIGNAL.				
SQ	SEQUENCE 212 AA; 24350 MW; 718A2C82 CRC32;				

Query Match 76.6%; Score 1375; DB 14; Length 212;
Best Local Similarity 99.5%; Pred. No. 9, 01e-219;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVLLSFLPSDFPSPVRLDLDITASALYREALSEPHCSPHHTALRQAI 88
:|||||
QY 57 SMDIDPYKEFGATVLLSFLPSDFPSPVRLDLDITASALYREALSEPHCSPHHTALRQAI 116
:|||||

Db 89 LCMGELMTLATVGVNLEDPASRDVLSVYNTNMGLKRFQOLMFHISCLTFGREVIEYL 148
:|||||
QY 117 LCMGELMTLATVGVNLEDPASRDVLSVYNTNMGLKRFQOLMFHISCLTFGREVIEYL 176
:|||||

Db 149 VSFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
:|||||
QY 177 VSFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 236
:|||||

Db 209 ESQC 212
:|||||
QY 237 ESQC 240

RESULT 2
ID Q68020 PRELIMINARY; PRT: 212 AA.
AC Q68020:
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTAG-1'85;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85291; G736119; -;
DR PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24336 MW; EDE4C243 CRC32;

Query Match 76.5%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 1, 37e-218;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVLLSFLPSDFPSPVRLDLDITASALYREALSEPHCSPHHTALRQAI 88
:|||||
QY 57 SMDIDPYKEFGATVLLSFLPSDFPSPVRLDLDITASALYREALSEPHCSPHHTALRQAI 116
:|||||

Db 89 LCMGELMTLATVGVNLEDPASRDVLSVYNTNMGLKRFQOLMFHISCLTFGREVIEYL 148
:|||||
QY 117 LCMGELMTLATVGVNLEDPASRDVLSVYNTNMGLKRFQOLMFHISCLTFGREVIEYL 176
:|||||

Db 149 VSFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
:|||||
QY 177 VSFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 236
:|||||

Db 209 ESQC 212
:|||||
QY 237 ESQC 240

RESULT 3
ID Q89597 PRELIMINARY; PRT: 212 AA.
AC Q89597:
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE HBCAG.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUB-TYPE AYW;

RX MEDLINE: 94079539.
RA PREISLER-ADAMS S., SCHLAYER M.J., PETERS T., HETTLER F., GEROK W.,
RA RASENCK J.;
RT "Sequence analysis of hepatitis B virus DNA in immunologically
RT negative infection."
RL ARCH. VIROL. 133:385-396(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-AYW;
RC SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X72702; G288930; -;
DR EMBL: X80925; E198084; -;
DR PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24336 MW; 575D20BF CRC32;

Query Match 76.5%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 1, 37e-218;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVLLSFLPSDFPSPVRLDLDITASALYREALSEPHCSPHHTALRQAI 88
:|||||
QY 57 SMDIDPYKEFGATVLLSFLPSDFPSPVRLDLDITASALYREALSEPHCSPHHTALRQAI 116
:|||||

Db 89 LCMGELMTLATVGVNLEDPASRDVLSVYNTNMGLKRFQOLMFHISCLTFGREVIEYL 148
:|||||
QY 117 LCMGELMTLATVGVNLEDPASRDVLSVYNTNMGLKRFQOLMFHISCLTFGREVIEYL 176
:|||||

Db 149 VSFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
:|||||
QY 177 VSFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 236
:|||||

Db 209 ESQC 212
:|||||
QY 237 ESQC 240

RESULT 4
ID Q89437 PRELIMINARY; PRT: 183 AA.
AC Q89437:
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (CASTA 2).
GN CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTA-2'87;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85289; G736113; -;
DR EMBL: X80925; E198085; -;
DR PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 183 AA; 21102 MW; 0C504D47 CRC32;

Query Match 76.4%; Score 1373; DB 14; Length 183;

Best Local Similarity 99.5%; Pred. No. 2.09e-218;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
|||
Qy 58 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 117
|||
Db 61 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLIMFHSICLTGRETVEYELV 120
|||
Qy 118 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLIMFHSICLTGRETVEYELV 177
|||
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
|||
Qy 178 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 237
|||

Db 181 SQC 183
|||
Qy 238 SQC 240

RESULT 5
ID 068008 PRELIMINARY; PRT: 183 AA.
AC 068008:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (FERRACUTI 1).
GN CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT FERRACUTI-1'89;
RA LAI M.E., MAZZOLENTI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X83284; G736098; -;
PRFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 183 AA; 21102 MW; BBE9AFBB CRC32;

Query Match 76.4%; Score 1373; DB 14; Length 183;
Best Local Similarity 99.5%; Pred. No. 2.09e-218;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
|||
Qy 58 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 117
|||
Db 61 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLIMFHSICLTGRETVEYELV 120
|||
Qy 118 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLIMFHSICLTGRETVEYELV 177
|||
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
|||
Qy 178 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 237
|||

Db 181 SQC 183
|||
Qy 238 SQC 240

RESULT 6
ID 067876 PRELIMINARY; PRT: 212 AA.
AC 067876:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE C/C ORF.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CI, HBV SUBTYPE AYW;
RA LAI M.E., MAZZOLENTI A.P., BALESTRIERI A., MELIS A., PORRU A.;

RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65258; G59436; -;
PRFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24348 MW; 6ED741BE CRC32;

Query Match 76.4%; Score 1373; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 2.09e-218;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
|||
Qy 57 GMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 116
|||
Db 89 LCWELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLIMFHSICLTGRETVEYELV 148
|||
Qy 117 LCWELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLIMFHSICLTGRETVEYELV 176
|||
Db 149 VAFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
|||
Qy 177 VAFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 236
|||

Db 209 ESOC 212
|||
Qy 237 ESOC 240

RESULT 7
ID 011884 PRELIMINARY; PRT: 212 AA.
AC 011884:
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN PRECURSOR.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA RAO B.S., CASEY J.L., RINAUDO J.S., KORBA B.E.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U95551; G2182120; -;
PRFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24360 MW; 73AC92DB CRC32;

Query Match 76.4%; Score 1372; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 3.18e-218;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
|||
Qy 57 GMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 116
|||
Db 89 LCWELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLIMFHSICLTGRETVEYELV 148
|||
Qy 117 LCWELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLIMFHSICLTGRETVEYELV 176
|||
Db 149 VAFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
|||
Qy 177 VAFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 236
|||

Db 209 ESOC 212
|||
Qy 237 ESOC 240

RESULT 8
ID 068066 PRELIMINARY; PRT: 183 AA.
AC 068066:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (LICHERI 2).
GN CORE.
OS HEPATITIS B VIRUS.


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QY      237 ESQC 240

RESULT 12
ID      067984
AC      067984
DT      01-NOV-1996 (TREMBLREL. 01, CREATED)
DT      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT      01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE      PRE-C/CORE.
GN      HEPATITIS B VIRUS.
OS      HEPATITIS B VIRUS.
OC      VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-PATIENT VITTORINA'92.
RA      LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL      SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR      EMBL: X85256; G736052; -.
PFAM: PF00906; Hepatitis_core: 1.
SQ      SEQUENCE 212 AA; 24322 MW; 83D9780B CRC32;

Query Match
Best Local Similarity 98.4%; Score 1369; DB 14; Length 212;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db      29 GMDIPYKEFGATVELLSFSPDFFPSVBDLDTASALYREALSEPHHIALROI 88
QY      :|||||
Db      57 SMDIPYKEFGATVELLSFSPDFFPSVBDLDTASALYREALSEPHHIALROI 116
QY      :|||||
Db      89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQOLMFHISCLTFGRETVIEYL 148
QY      117 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQOLMFHISCLTFGRETVIEYL 176
QY      149 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY      177 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 236
Db      209 ESQC 212
QY      237 ESQC 240

RESULT 13
ID      068032
AC      068032
DT      01-NOV-1996 (TREMBLREL. 01, CREATED)
DT      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT      01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE      PRE-C/CORE.
GN      HEPATITIS B VIRUS.
OS      HEPATITIS B VIRUS.
OC      VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-PATIENT CHICHINE-2'86;
RA      LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL      SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR      EMBL: X85296; G736139; -.
PFAM: PF00906; Hepatitis_core: 1.
SQ      SEQUENCE 212 AA; 24308 MW; 69D87B53 CRC32;

Query Match
Best Local Similarity 98.4%; Score 1369; DB 14; Length 212;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db      29 GMDIPYKEFGATVELLSFSPDFFPSVBDLDTASALYREALSEPHHIALROI 88
QY      :|||||
Db      57 SMDIPYKEFGATVELLSFSPDFFPSVBDLDTASALYREALSEPHHIALROI 116
QY      :|||||
Db      89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQOLMFHISCLTFGRETVIEYL 148
QY      117 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQOLMFHISCLTFGRETVIEYL 176
QY      149 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY      177 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 236
Db      209 ESQC 212
QY      237 ESQC 240

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QY      117 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQOLMFHISCLTFGRETVIEYL 176
Db      149 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY      177 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 236
Db      209 ESQC 212
QY      237 ESQC 240

RESULT 14
ID      068010
AC      068010
DT      01-NOV-1996 (TREMBLREL. 01, CREATED)
DT      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT      01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE      PRE-C/CORE.
GN      HEPATITIS B VIRUS.
OS      HEPATITIS B VIRUS.
OC      VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-PATIENT FERRACUTI-2'90;
RA      LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL      SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR      EMBL: X85285; G736100; -.
PFAM: PF00906; Hepatitis_core: 1.
SQ      SEQUENCE 212 AA; 24292 MW; 04A4D12D CRC32;

Query Match
Best Local Similarity 98.4%; Score 1368; DB 14; Length 212;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db      29 GMDIPYKEFGATVELLSFSPDFFPSVBDLDTASALYREALSEPHHIALROI 88
QY      :|||||
Db      57 SMDIPYKEFGATVELLSFSPDFFPSVBDLDTASALYREALSEPHHIALROI 116
QY      :|||||
Db      89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQOLMFHISCLTFGRETVIEYL 148
QY      117 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQOLMFHISCLTFGRETVIEYL 176
QY      149 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY      177 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRRRTSPRRRSQSPRRRSQSR 236
Db      209 ESQC 212
QY      237 ESQC 240

RESULT 15
ID      068070
AC      068070
DT      01-NOV-1996 (TREMBLREL. 01, CREATED)
DT      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT      01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE      PRE-C/CORE.
GN      HEPATITIS B VIRUS.
OS      HEPATITIS B VIRUS.
OC      VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-PATIENT GIORDO'84;
RA      LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL      SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR      EMBL: X85316; G736210; -.
PFAM: PF00906; Hepatitis_core: 1.
SQ      SEQUENCE 212 AA; 24376 MW; 80F52D0F CRC32;

Query Match
Best Local Similarity 98.1%; Score 1366; DB 14; Length 212;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db      29 GMDIDPYKFGATVELLSFLPSDFPSPVROLDLTASALYREALSPHCHSPHHTALROAI 88
QY      57 SMDIDPYKFGATVELLSFLPSDFPSPVROLDLTASALYREALSPHCHSPHHTALROAI 116
Db      89 LCMGELMTLATWGVNLEDPAASRDVVSNTNMGKFRQLMFHISCLTFGRETVEYL 148
QY     117 LCMGELMTLATWGVNLEDPAASRDVVSNTNMGKFRQLMFHISCLTFGRETVEYL 176
Db     149 VSEGVWIRTPPAIRPPNAPILTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY     177 VSEGVWIRTPPAIRPPNAPILTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 236
Db     209 ESQC 212
QY     237 ESQC 240

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Search completed: Thu Dec 16 13:16:01 1999
 Job time : 98 secs.

 M O S E I N
 (TM)

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Msrch_lp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Dec 16 13:20:19 1999; MasPar time 12.84 Seconds
 Tabular output not generated. 460.333 Million cell updates/sec

Title: >US3869-29-38183
 Description: (1-278) from us3869-29-38183.pep
 Perfect Score: 2088
 Sequence: 1 MDIDPYKEFGATVELLSFLP.....RRRRSQSPRRRSQSRSSOC 278
 Scoring table: PAM 150
 Gap 11

Searched: 170751 seqs, 21266608 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 33.381; Variance 171.697; scale 0.194

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1375	65.9	194	32	W50242	Hepatitis B virus pre
2	1375	65.9	212	32	W50250	Hepatitis B virus pre
3	1375	65.9	346	5	R27473	S12/core protein.
4	1363	65.1	184	1	P80959	Hepatitis B virus sub
5	1359	65.1	193	32	W50241	Hepatitis B virus pre
6	1358	65.0	183	32	W50251	Hepatitis B virus p21
7	1353	64.8	183	20	W09044	Hepatitis B virus cor
8	1349	64.6	183	1	R05635	Hepatitis B antigen.
9	1349	64.6	183	5	P00041	Sequence of core anti
10	1344	64.4	397	20	W09048	Plasmid pHEV DN Aa en
11	1338	64.1	184	5	P00004	Sequence of core anti
12	1336	64.0	196	8	R40806	Hepatitis B core / PV
13	1337	63.9	208	8	R40808	Hepatitis B core / PV
14	1334	63.9	183	4	R40311	Hepatitis B virus core
15	1334	63.9	183	8	R40805	Hepatitis B virus core
16	1334	63.9	183	13	R68868	Hepatitis B virus pol

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
17	1334	63.9	183	12	R62869	Hepatitis B virus core
18	1333	63.8	198	8	R40807	Hepatitis B core / IL
19	1328	63.6	293	10	R52866	Pres1 full length cor
20	1325	63.5	183	13	R68866	Hepatitis B virus pol
21	1325	63.5	214	1	P90702	Deduced amino acid se
22	1325	63.5	289	20	W09049	Plasmid pHEV DN BB en
23	1324	63.4	185	6	R30861	Hepatitis B core anti
24	1324	63.4	185	10	R55284	Deduced sequence of f
25	1324	63.4	185	6	R30780	Native HBcAg protein.
26	1324	63.4	185	6	R30780	Native HBcAg protein.
27	1321	63.3	185	26	P30061	Core antigen of HBV.
28	1320	63.2	183	13	R68869	Hepatitis B virus pol
29	1317	63.1	185	6	R30781	Altered HBcAg protein
30	1317	63.1	185	6	R31026	Altered HBcAg protein
31	1314	62.9	183	13	R68867	Hepatitis B virus pol
32	1313	62.9	183	13	R68870	Hepatitis B virus pol
33	1311	62.8	185	6	R30784	Altered HBcAg protein
34	1311	62.8	185	6	R31029	Altered HBcAg protein
35	1311	62.8	185	6	R30865	Modified hepatitis B
36	1309	62.7	185	6	R30862	Hepatitis B core anti
37	1308	62.6	185	6	R30783	Altered HBcAg protein
38	1308	62.6	185	6	R30864	Modified hepatitis B
39	1308	62.6	185	6	R30864	Modified hepatitis B
40	1302	62.4	203	1	P82872	HBcAg/beta-Gal fusion
41	1303	62.4	214	1	P80961	HBV core antigen enco
42	1287	61.6	198	32	W50252	Hepatitis B virus pre
43	1263	60.5	183	17	R98878	Hepatitis B virus E a
44	1259	60.3	183	17	R98883	Hepatitis B virus E a
45	1258	60.2	183	17	R98884	Hepatitis B virus E a

ALIGNMENTS

RESULT 1
 ID W50242: standard; Protein; 194 AA.

DT 28-SEP-1998 (first entry)
 DE Hepatitis B virus precore p22 polypeptide Met-p22.
 KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
 KW hepatocyte; liver; Met-p22.

OS Hepatitis B virus.
 OS Synthetic.

FT Key
 FT Location/Qualifiers
 FT 2..194
 FT /label= p22

PN W09809649-A1.

PD 12-MAR-1998.

PF 03-SEP-1997; U15500.

PR 03-SEP-1996; US-025370.

PA (GCHO) GEN HOSPITAL CORP.

PI Melegari M, Scaglioni PP, Wands JR;
 WPI: 98-193325/17

DR DNA encoding proteins which can be incorporated with wild type

PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for

FT inhibition of viral replication, especially hepatitis B virus

PS Claim 11; Page 40; 60pp; English.

CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)

CC protein with an added N-terminal Met residue. p22 is produced by

CC elimination of the 19-amino acid leader peptide from the 25 kDa

CC full-length HBV precore protein (see W50250). Evidence is provided

CC that HBV replication is inhibited in the presence of high levels of

CC HBV precore or precore-related proteins. These proteins can be

CC incorporated into HBV nucleocapsids along with the p1 core protein

CC (see W50251), which is the usual nucleocapsid component, and HBV

CC thereby render the nucleocapsids deficient in encapsidating HBV

CC pregenomic RNA. Thus, over-expression of the precore proteins, or

CC certain variants of them, leads to transdominant inhibition of HBV

CC replication. Suitable inhibitory proteins include p25 (see W50250),

CC p22, Met-p22, p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het

CC (see W50338). Heterologous peptides (see W50244-49) may be

CC inserted into the p22 and Met-p22 polypeptides. The inhibitory

CC proteins can be produced by recombinant methods using claimed

CC expression vectors and host cells. They can be provided exogenously

CC to the target cells for use in inhibiting HBV replication.
 CC Alternatively, a nucleic acid construct that directs overexpression
 CC of an inhibitory protein in target cells is used for the gene
 CC therapy of HBV infection.
 SQ Sequence 194 AA;

Query Match 65.9%; Score 1375; DB 32; Length 194;
 Best Local Similarity 99.5%; Pred. No. 1.04e-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 gmidpkykefgatvelsfpsdfpsvrdlltdasalyreallespschphntalrqt 70
 :|||||
 QY 95 SMDIDPKKEGATVELLSFSDFFPSVRLDLSALYREALLESPPHNTALRQAI 154
 :|||||
 Db 71 lwcgelmclatwgvnlcdpasrdlvsyvtntmgjkfgrllwfhisccltfgretvleyl 130
 :|||||
 QY 155 LCMGELMTLATWGVNLCDPASRDLVSYVTNTMGKLFRLMLFHSICLFGRETVEYL 214
 :|||||
 Db 131 vsfgvwlrtppayrppnaillstlpetvtvrrrgsprrrrrsgsprrrrrsgsr 190
 :|||||
 QY 215 VSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 274
 :|||||
 Db 191 esgc 194
 :|||||
 QY 275 ESQC 278

RESULT 2

ID W50250 standard; Protein: 212 AA.
 AC W50250:
 DT 28-SEP-1998 (first entry)
 DE Hepatitis B virus precore p25 polypeptide.
 KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
 KW hepatocyte; liver; p25 protein.
 OS Hepatitis B virus.
 PN MO9809649-A1.
 PD 12-MAR-1998.
 PE 03-SEP-1997; 015500.
 PR 03-SEP-1996; US-025370.
 PA (GENE) GEN HOSPITAL CORP.
 PI Melegari M, Scagliola PP, Wands JR;
 DR WPI: 98-193325/17
 PT DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus
 PS Claim 15: Page 35; 60pp; English.
 CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)
 CC protein that is encoded by the full-length HBV precore gene.
 CC Evidence is provided that HBV replication is inhibited in the
 CC presence of high levels of HBV precore or precore-related proteins.
 CC These proteins can be incorporated into HBV nucleocapsids along
 CC with the p21 core protein (see W50251), which is the usual
 CC nucleocapsid component, and thereby render the nucleocapsids
 CC deficient in encapsitating HBV pregenomic RNA. Thus, over-
 CC expression of the precore proteins, or certain variants of them,
 CC leads to transdominant inhibition of HBV replication. Suitable
 CC inhibitory proteins include p25, p22 (see W50241), Met-p22 (see
 CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
 CC (see W50238). The inhibitory proteins can be produced by
 CC recombinant methods using claimed expression vectors and host
 CC cells. They can be provided exogenously to the target cells for
 CC use in inhibiting HBV replication. Alternatively, a nucleic acid
 CC construct that directs overexpression of an inhibitory protein in
 CC target cells is used for the gene therapy of HBV infection.
 SQ Sequence 212 AA;

Query Match 65.9%; Score 1375; DB 32; Length 212;
 Best Local Similarity 99.5%; Pred. No. 1.04e-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 gmidpkykefgatvelsfpsdfpsvrdlltdasalyreallespschphntalrqt 88
 :|||||
 QY 95 SMDIDPKKEGATVELLSFSDFFPSVRLDLSALYREALLESPPHNTALRQAI 154
 :|||||

Db 89 lwcgelmclatwgvnlcdpasrdlvsyvtntmgjkfgrllwfhisccltfgretvleyl 148
 :|||||
 QY 155 LCMGELMTLATWGVNLCDPASRDLVSYVTNTMGKLFRLMLFHSICLFGRETVEYL 214
 :|||||

Db 149 vsfgvwlrtppayrppnaillstlpetvtvrrrgsprrrrrsgsprrrrrsgsr 208
 :|||||
 QY 215 VSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 274
 :|||||

Db 209 esgc 212
 :|||||
 QY 275 ESQC 278

RESULT 3

ID R27473 standard; Protein: 346 AA.
 AC R27473:
 DT 24-FEB-1993 (first entry)
 DE S12/core protein.
 KW Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
 KW vaccinia virus; I3L; promoter; NVVAC; recombinant; HBV L;
 KW large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;
 KW S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;
 KW deletion loci; recipient loci.
 OS Synthetic.
 FH Key
 FT region
 FT location/Qualifiers
 FT 1..108
 FT /label S1
 FT region 109..163
 FT /label S2
 FT region 164..346
 FT /label Core
 PN WO9215672-A.
 PD 17-SEP-1992.
 PE 09-MAR-1992; 001906.
 PR 07-MAR-1991; US-666056.
 PR 11-JUN-1991; US-713967.
 PR 06-MAR-1992; US-847951.
 PA (VIRO-) VIROGENETICS CORP.
 PI Cox WI, De Taisne C, Francis J, Gettig RR, Johnson GP,
 PI Limbach KJ, Norton EK, Paoletti E, Perkins ME, Plincus SE,
 PI Riviere M, Tartaglia J, Taylor J;
 DR WPI: 92-331718/40.
 DR N-PSDB: Q29105.
 PT Vaccine comprises recombinant, attenuated pox-virus - use for
 PT vaccinating against viral infections such as rabies, hepatitis B,
 PT HIV, HSV, EBV, CMV, mumps etc.
 PS Disclosure: Fig 13; 45pp; English.
 CC The sequence given is encoded by an expression cassette which
 CC comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/
 CC core) which is precisely linked to the 13L promoter derived from
 CC vaccinia virus. This DNA sequence was linked to the S1 and S2
 CC sequences and this fragment was used in the construction of a NVVAC
 CC recombinant expressing the HBV gene. Other HBV genes were also used
 CC in the construction. These were HBV M protein (small pre-S antigen,
 CC spsAg) and HBV L (large pre-S antigen, lpsAg). Each of these gene
 CC sequences were inserted individually into three different sites of
 CC NVVAC separated by from each other by large regions of vaccinia DNA
 CC containing essential genes. NVVAC is a Copenhagen vaccine strain of
 CC vaccinia virus which has been modified by deletion of six non-essential
 CC regions of the genome encoding known or potential virulence factors.
 CC The deletion loci were engineered as recipient loci for the insertion
 CC of foreign genes. The spacing of the three inserted sequences ensured
 CC that any recombination that did occur would lead to disruption of the
 CC vaccinia genome and would cause unviable vaccinia virus. See also
 CC Q35501-864.
 SQ Sequence 346 AA;

Query Match 65.9%; Score 1375; DB 5; Length 346;
 Best Local Similarity 99.5%; Pred. No. 1.04e-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 163 mmidpkykefgatvelsfpsdfpsvrdlltdasalyreallespschphntalrqt 222
 :|||||

QY 216 SFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 274

RESULT 11

ID P00004 standard: Protein; 184 AA.
AC P00004;
DT 14-OCT-1992 (first entry)
DE Sequence of core antigen.
KW Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
OS Hepatitis B virus.
PN EP-13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979; 303017.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOJ) BIOGEN NV.
PI Murray K, Schaller HE;
DR WPI; 80-57288C/33.
DR N-PSDB; N00002.
PT Recombinant DNA coding for polypeptide - have specificity of
PS hepatitis B viral antigens in detection or antibody stimulation
PS Claim 13; Page 40; 43pp; English.
CC Human serum from a single HBsAg positive, HBeAg positive donor
CC (serotype adym) was used to prep. a DNA-contg. pellet which was
CC labeled with 3H or 32P as described by P. M. Kaplan et al (1973).
CC The labeled DNA was then extracted with phenol from the resulting
CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
CC It was then cloned in plasmid pBR322 which was used to transform E.
CC coli. Micro-organisms prepd. by the processes are deposited at the
CC NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst 1 dg;
CC HBV-Kpn I dc; Tetr Amps HBV+.
SQ Sequence 184 AA:

Query Match 64.1%; Score 1338; DB 5; Length 184;
Best Local Similarity 96.2%; Pred. No. 1.19e-97;

Matches 177; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

DB 1 mdidpykefagavellsfpsdfpsvordlldtaaalrydalespeshphthalrgai 60
QY 96 MDIDPYKEFAGAVELLSFPSDFPSV-RDLDLTAALRYDALESPEHCSPHTALRQAI 154
DB 61 lcgwglmrlatwgvnledpasrdlvsvyvtngmkfrolmhfhscltfgretvleyl 120
QY 155 LCGWGLMRLATWGVNLEDPASRDLVSVYVTNGMKFROLMHFHISCLTFGRETVLEYL 214
DB 121 vsfgvwtirtppayrppnapilstlpetvrrgrsprrrtsprrrsqsprrrsqsr 180
QY 215 VSFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 274
DB 181 esgc 184
QY 275 ESQC 278

RESULT 12

ID R40806 standard: Protein; 196 AA.
AC R40806;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 fusion.
KW Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Synthetic.
FH Key
FT region 7..13
FT protein /label= PV-1
FT 14..196
FT /label= HBC

J05192170-A.
PN 03-AUG-1993.
PF 24-SEP-1991; 243800.
PR 24-SEP-1991; JP-243800.
RA (NISW) NISSHIN OIL MILLS LTD.

DR WPI; 93-277479/35.

DR N-PSDB; Q47736.
PT Recombinant plasmid for high immunogenicity virus - contains
PT recombinant haemagglutinin gene, hepatitis B core gene of vaccinia
PT virus and exotic genes
PS Disclosure: Fig 7; 12pp; Japanese.
CC The hepatitis B core gene is recombined with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
SQ Specification.
SQ Sequence 196 AA:

Query Match 64.0%; Score 1336; DB 8; Length 196;
Best Local Similarity 95.1%; Pred. No. 1.74e-97;
Matches 175; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

DB 13 amdidpykefagavellsfpsdfpsvordlldtaaalrydalespeshphthalrgai 72
QY 95 SMIDPYKEFAGAVELLSFPSDFPSVORDLDLTAALRYDALESPEHCSPHTALRQAI 154
DB 73 lcgwglmrlatwgvnledpasrdlvsvyvtngmkfrolmhfhscltfgretvleyl 132
QY 155 LCGWGLMRLATWGVNLEDPASRDLVSVYVTNGMKFROLMHFHISCLTFGRETVLEYL 214
DB 133 vsfgvwtirtppayrppnapilstlpetvrrgrsprrrtsprrrsqsprrrsqsr 192
QY 215 VSFGVWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 274
DB 193 esgc 196
QY 275 ESQC 278

RESULT 13
ID R40806 standard: Protein; 208 AA.
AC R40806;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 / IL-1 fusion.
KW Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Synthetic.
FH Key
FT region 8..19
FT protein /label= PV-1
FT 20..25
FT /label= IL-1
FT 26..208
FT /label= HBC

J05192170-A.
PN 03-AUG-1993.
PF 24-SEP-1991; 243800.
PR 24-SEP-1991; JP-243800.
PA (NISW) NISSHIN OIL MILLS LTD.
DR WPI; 93-277479/35.
DR N-PSDB; Q47738.
PT Recombinant plasmid for high immunogenicity virus - contains
PT recombinant haemagglutinin gene, hepatitis B core gene of vaccinia
PT virus and exotic genes
PS Disclosure: Fig 9; 12pp; Japanese.
CC The hepatitis B core gene is recombined with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
SQ Specification.
SQ Sequence 208 AA:

Query Match 64.0%; Score 1337; DB 8; Length 208;
Best Local Similarity 94.6%; Pred. No. 1.44e-97;
Matches 175; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

DB 24 lcgwglmrlatwgvnledpasrdlvsvyvtngmkfrolmhfhscltfgretvleyl 143
QY 94 LSMDIDPYKEFAGAVELLSFPSDFPSVORDLDLTAALRYDALESPEHCSPHTALRQAI 153
DB 84 lcgwglmrlatwgvnledpasrdlvsvyvtngmkfrolmhfhscltfgretvleyl 143

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QY 154 ILGELMTLATWGVNLEDPASRDLVSYVNTNGLFROLWHISCLTFGRETVEY 213
DB 144 LVSGVWIRTPPAYRPPNAPILSTLPETVVRIGRSPRRTPSPRRISQSGS 203
QY 214 LVSGVWIRTPPAYRPPNAPILSTLPETVVRIGRSPRRTPSPRRISQSGS 273
DB 204 resgc 208
QY 274 RESQC 278

RESULT 14
ID P40311 standard; Protein; 183 AA.
AC P40311;
DT 18-AUG-1992 (first entry)
DE Hepatitis virus core antigen.
KM HBCAg; vaccine; diagnosis; HBV infection.
OS Hepatitis B virus.
PN J59074985-A.
PD 27-APR-1984.
PF 19-OCT-1982; 183432.
PR 19-OCT-1982; JP-183432.
PA (TAKE ) TAKEDA CHEMICAL IND KK.
DR WPI; 84-14321/23.
PT DNA used in prevention of infections by hepatitis virus B -
  comprises structural gene of hepatitis virus adr B surface antigen
  coding gene and at least 1 virus core antigen structural gene.
PS Disclosure; Fig 3; 13pp; Japanese.
CC The sequence is that of hepatitis virus core antigen (HBCAg). It
  can be used as a vaccine for the prevention of infections by
  hepatitis B virus (HBV) and also in the diagnosis of early stages
  of HBV infection. See also P40310.
SQ Sequence 183 AA.

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```

Query Match 63.9%; Score 1334; DB 4; Length 183;
Best Local Similarity 95.6%; Pred. No. 2.55e-97;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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DB 1 mdidpykefgasvvelsfpsdfffpsirdlidsasalyrealsepncsphthalrgail 60
QY 96 MDIDPYKEFGATVELSLFSPDFPSVVDLDTASALYREALSEPNCSPHHTALRQAIL 155
DB 61 CWGELMTLATWGVNLEDPASRDLVSYVNTNGLFROLWHISCLTFGRETVEYLV 120
QY 156 CWGELMTLATWGVNLEDPASRDLVSYVNTNGLFROLWHISCLTFGRETVEYLV 215
DB 121 sfgywlrtppayrppnapilstlpetvvrigrsprrtpsprrisqsgsre 180
QY 216 SFGVWIRTPPAYRPPNAPILSTLPETVVRIGRSPRRTPSPRRISQSGSRE 275
DB 181 sqc 183
QY 276 SQC 278

```

```

RESULT 15
ID R40805 standard; Protein; 183 AA.
AC R40805;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core protein.
KM Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Hepatitis B virus.
PN J05192170-A.
PD 03-AUG-1993.
PF 24-SEP-1991; 243800.
PR 24-SEP-1991; JP-243800.
PA (NISW ) NISSHIN OIL MILLS LTD.
DR WPI; 93-277479/35.
PT Recombinant plasmid for high immunogenity virus - contains
  recombinant haemagglutinin gene, hepatitis B core gene of vaccinia
  virus and exotic genes

```

```

PS Disclosure; Fig 6; 12pp; Japanese.
CC The hepatitis B core gene is recombined with PV-1 DNA
  and IL-1 beta to form a plasmid (Q47738) which is then used to produce
  a vaccine. NB: Sequence is difficult to read in the original
  CC specification.
SQ Sequence 183 AA;

```

```

Query Match 63.9%; Score 1334; DB 8; Length 183;
Best Local Similarity 95.6%; Pred. No. 2.55e-97;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

DB 1 mdidpykefgasvvelsfpsdfffpsirdlidsasalyrealsepncsphthalrgail 60
QY 96 MDIDPYKEFGATVELSLFSPDFPSVVDLDTASALYREALSEPNCSPHHTALRQAIL 155
DB 61 CWGELMTLATWGVNLEDPASRDLVSYVNTNGLFROLWHISCLTFGRETVEYLV 120
QY 156 CWGELMTLATWGVNLEDPASRDLVSYVNTNGLFROLWHISCLTFGRETVEYLV 215
DB 121 sfgywlrtppayrppnapilstlpetvvrigrsprrtpsprrisqsgsre 180
QY 216 SFGVWIRTPPAYRPPNAPILSTLPETVVRIGRSPRRTPSPRRISQSGSRE 275
DB 181 sqc 183
QY 276 SQC 278

```

```

Search completed: Thu Dec 16 13:23:42 1999
Job time : 203 secs.

```


US3869-29-38183
MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCHSPHHTALROAILCWEGLMTL
DGFLLLOMDGFEPEHLVDLQSLSDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSP
EHCSPHHTALROAILCWEGLMTLWGVNLEDPASRDVVSYNWGLKFRQLWPHISCLTFGRETV
IEXLVSGWVIRTPPARPPNAPILSTLPETTVRRGRSPRRRTSPRRRSOSPRRRRSOSRESOCI

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Msrch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 13:23:59 1999; Maspar time 13.87 Seconds
Tabular output not generated.

(TW)

Title: >US3869-29-38183
Description: (1-278) from us3869-29-38183.pep
Perfect Score: 2088
Sequence: 1 MDIDPKKEGATVELLSFLP.....RRRRSQSPRRRSQSHESOC 278

Scoring table:

PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

p1r60
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 46.997; Variance 115.318; scale 0.408

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1375	65.9	212	1	NKVLAH e antigen precursor / 4.25e-205	
2	1373	65.8	183	2	S53207 e antigen - hepati 9.36e-205	
3	1374	65.8	212	2	S53211 e antigen precursor / 6.31e-205	
4	1374	65.8	212	2	S32204 e antigen precursor / 6.31e-205	
5	1373	65.8	212	2	S20750 e antigen precursor / 9.36e-205	
6	1370	65.6	183	2	S53270 core antigen - hepati 3.06e-204	
7	1370	65.6	212	2	S53216 e antigen precursor / 3.06e-204	
8	1370	65.6	212	2	S53272 e antigen precursor / 3.06e-204	
9	1369	65.6	212	2	S53163 e antigen precursor / 4.53e-204	
10	1369	65.6	212	2	S20746 e antigen precursor / 4.53e-204	
11	1369	65.6	212	2	S53225 e antigen precursor / 4.53e-204	
12	1368	65.5	212	2	S53198 e antigen precursor / 6.72e-204	
13	1366	65.4	212	2	S53223 e antigen precursor / 1.48e-203	
14	1366	65.4	212	2	S53274 e antigen precursor / 1.48e-203	
15	1364	65.3	183	2	S53169 core antigen - hepati 3.26e-203	
16	1363	65.3	183	2	S53247 core antigen - hepati 4.83e-203	
17	1363	65.3	212	2	S53202 e antigen precursor / 4.83e-203	
18	1363	65.3	212	2	S53159 e antigen precursor / 4.83e-203	
19	1363	65.3	212	2	S53200 e antigen precursor / 4.83e-203	
20	1362	65.2	212	2	S53251 e antigen precursor / 7.16e-203	
21	1360	65.1	212	2	S53204 e antigen precursor / 1.58e-202	
22	1360	65.1	212	2	S53227 e antigen precursor / 1.58e-202	
23	1359	65.1	212	2	S53253 e antigen precursor / 2.34e-202	

ENTRY TITLE	ALTERNATE_NAMES CONTAINS ORGANISM #variety	ALIGNMENTS
24 1358 65.0 211 1 NKVLAH	#type complete	e antigen precursor / 3.47e-202
25 1357 65.0 212 2 S53281	e antigen precursor / core antigen - hepatitis B virus	e antigen precursor / 5.14e-202
26 1355 64.9 212 1 NKVLBH	HBe antigen precursor / HBe antigen; pre-C/C antigen	e antigen precursor / 1.13e-201
27 1355 64.9 212 2 S53242	core antigen; e antigen	e antigen precursor / 1.13e-201
28 1351 64.7 183 2 S53129	core antigen - hepati	core antigen - hepati 5.47e-201
29 1351 64.7 212 2 S53240	e antigen precursor /	e antigen precursor / 5.47e-201
30 1349 64.6 183 1 NKVLAA	core antigen - hepati	core antigen - hepati 1.20e-200
31 1349 64.6 183 2 S53181	core antigen - hepati	core antigen - hepati 1.20e-200
32 1348 64.6 183 2 S53232	core antigen - hepati	core antigen - hepati 1.79e-200
33 1348 64.6 183 2 S53260	core antigen - hepati	core antigen - hepati 1.79e-200
34 1345 64.4 183 2 S53152	core antigen - hepati	core antigen - hepati 5.82e-200
35 1344 64.4 212 2 S53229	e antigen precursor /	e antigen precursor / 8.64e-200
36 1343 64.3 183 2 S53214	core antigen - hepati	core antigen - hepati 1.28e-199
37 1342 64.3 183 2 S53140	core antigen - hepati	core antigen - hepati 1.90e-199
38 1341 64.2 183 2 S53267	core antigen - hepati	core antigen - hepati 2.82e-199
39 1341 64.2 183 2 S53189	core antigen - hepati	core antigen - hepati 2.82e-199
40 1341 64.2 212 2 S53238	e antigen precursor /	e antigen precursor / 2.82e-199
41 1340 64.2 212 2 S53257	e antigen precursor /	e antigen precursor / 4.18e-199
42 1339 64.1 183 2 S53137	core antigen - hepati	core antigen - hepati 6.19e-199
43 1339 64.1 212 2 S53651	e antigen precursor /	e antigen precursor / 6.19e-199
44 1338 64.1 212 2 S53236	e antigen precursor /	e antigen precursor / 9.18e-199
45 1337 64.0 212 1 NKVLJ2	e antigen precursor /	e antigen precursor / 1.36e-198

REFERENCE #authors #submitted to the EMBL Data Library, August 1994
#description Molecular cloning and sequencing of two complete genomes of
#accession S47405
#molecule_type DNA
#residues 1-212 #label PLU
#cross-references EMBL:235716; NID:g527435; PID:g527437
#experimental_source subtype ayw4, isolate hb321

REFERENCE #authors #submitted to the EMBL Data Library, March 1995
#accession S53191
#molecule_type DNA
#residues 1-212 #label LA1
#cross-references EMBL:X85283; NID:g736088; PID:g736090
#experimental_source isolate patient Ferracuti 83

#accession S53209
#molecule_type DNA
#residues 1-212 #label LA2
#cross-references EMBL:X85290; NID:g736114; PID:g736116
#experimental_source isolate patient Castag 83

#accession S53234
#molecule_type DNA
#residues 1-212 #label LA3
#cross-references EMBL:X85300; NID:g736150; PID:g736152
#experimental_source isolate patient Sanna 84

#accession S53264
#molecule_type DNA
#residues 1-212 #label LA4
#cross-references EMBL:X85313; NID:g736194; PID:g736196

```
##experimental_source isolate patient Licheri-1'85
#accession S53249
##molecule_type DNA
##residues 1-212 ##label LA5
##cross-references EMBL:X85306; NID:g736172; PID:g736174
##experimental_source isolate patient Flore-1'86
#accession S53262
##molecule_type DNA
##residues 1-212 ##label LA6
##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
#accession S53277
##molecule_type DNA
##residues 30-212 ##label LA7
##cross-references EMBL:X85317; NID:g736211; PID:g736214
##experimental_source isolate patient Giordano-2'86
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be processed

REFERENCE A93214
#authors Galibert, F.; Mandart, E.; Fickoussi, F.; Tiollais, P.;
#journal Nature (1979) 281:646-650
#title Nucleotide sequence of the hepatitis B virus genome (subtype
#cross-references MIMD:81012091
#accession A03711
##molecule_type DNA
##residues 1-212 ##label GAL
##cross-references GB:J02203; NID:g329640; PID:g329642
#experimental_source subtype ayw

GENETICS
#gene C
#classification #superfamily hepatitis B virus core antigen
#keywords alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular_weight 24350 #checksum 782

Query Match 65.9%; Score 1375; DB 1; Length 212;
Best Local Similarity 99.5%; Pred. No. 4.25e-205;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||
QY 95 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 154
:|||||

Db 89 LCMGELMTLATWGVNEDPASRDVSVYNTNMGKFRQLMFMHISCLTFGRTVIEYL 148
:|||||
QY 155 LCMGELMTLATWGVNEDPASRDVSVYNTNMGKFRQLMFMHISCLTFGRTVIEYL 214
:|||||

Db 149 VSEGVWIRTPPAYRPPNAPILSTPETTVARRGRSPRRRSPRRRSOSPRRRRSOSR 208
:|||||
QY 215 VSEGVWIRTPPAYRPPNAPILSTPETTVARRGRSPRRRSPRRRSOSPRRRRSOSR 274
:|||||

Db 209 ESOC 212
:|||||
QY 275 ESOC 278

RESULT 2
ENTRY S53207 #type complete
TITLE core antigen - hepatitis B virus (isolate patient
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Castaa-2'87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997
```

```
ACCESSIONS S53207
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53207
##molecule_type DNA
##residues 1-183 ##label LA1
##cross-references EMBL:X85289; NID:g736110; PID:g736113
##experimental_source isolate patient Castaa-2'87
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
#classification #superfamily hepatitis B virus core antigen
#keywords core protein
SUMMARY #length 183 #molecular_weight 21102 #checksum 2165

Query Match 65.8%; Score 1373; DB 2; Length 183;
Best Local Similarity 99.5%; Pred. No. 9.36e-205;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 60
:|||||
QY 96 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 155
:|||||

Db 61 CMGELMTLATWGVNEDPASRDVSVYNTNMGKFRQLMFMHISCLTFGRTVIEYL 120
:|||||
QY 156 CMGELMTLATWGVNEDPASRDVSVYNTNMGKFRQLMFMHISCLTFGRTVIEYL 215
:|||||

Db 121 SFGVWIRTPPAYRPPNAPILSTPETTVARRGRSPRRRSPRRRSOSPRRRRSOSRE 180
:|||||
QY 216 SFGVWIRTPPAYRPPNAPILSTPETTVARRGRSPRRRSPRRRSOSPRRRRSOSRE 275
:|||||

Db 181 SOC 183
:|||||
QY 276 SOC 278

RESULT 3
ENTRY S53211 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Castag-1'85 and others)
ALTERNATE_NAMES HBC antigen; Hbc antigen precursor / Hbc antigen; pre-C/C
CONTAINS core antigen; e antigen
#formal_name hepatitis B virus, HBV
#isolate patient Castag-1'85; isolate patient Ferracuti-1'89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53211; S53197
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53211
##molecule_type DNA
##residues 1-212 ##label LA1
##cross-references EMBL:X85291; NID:g736117; PID:g736119
##experimental_source isolate patient Castag-1'85
#accession S53197
##molecule_type DNA
##residues 30-212 ##label LAW
##cross-references EMBL:X85284; NID:g736095; PID:g736098
##experimental_source isolate patient Ferracuti-1'89
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
#classification #superfamily hepatitis B virus core antigen
#keywords alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
179-212 #product e antigen #status predicted #label EAG\
```

179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP
SUMMARY #length 212 #molecular-weight 24336 #checksum 746

Query Match 65.8%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 6,31e-205;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALROAI 88
OY 95 SMDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALROAI 154

Db 89 LCMGELMTLATVGVNLEDPASRDVSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 148
OY 155 LCMGELMTLATVGVNLEDPASRDVSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 214

Db 149 VSGFWIRTPPAYRPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
OY 215 VSGFWIRTPPAYRPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 274

Db 209 ESQC 212
OY 275 ESQC 278

RESULT 4
ENTRY S32204 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C1000)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety subtype ayw, patient C1000
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS S32204
REFERENCE S32202
AUTHORS Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Gerox, W.; Rasmack, J.
#submission submitted to the EMBL Data Library, March 1993
#description identification and sequence analysis of hepatitis B virus DNA in immunological negative infection.
#accession S32204
#molecule_type DNA
#residues 1-212 #label PRE
#cross_references EMBL:X72702; NID:9288927; PID:9288930
#experimental_source subtype ayw, patient C1000
#note due to a stop codon between the alternative initiators the e antigen precursor cannot be produced

GENETICS C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
FEATURE 1-29
1-29 #domain signal sequence #status predicted #label SIG
30-212 #product core antigen #status predicted #label CAG
30-178 #product e antigen #status predicted #label EAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24336 #checksum 770

Query Match 65.8%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 6,31e-205;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALROAI 88
OY 95 SMDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALROAI 154

Db 89 LCMGELMTLATVGVNLEDPASRDVSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 148
OY 155 LCMGELMTLATVGVNLEDPASRDVSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 214

Db 149 VSGFWIRTPPAYRPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
OY 215 VSGFWIRTPPAYRPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 274

Db 209 ESQC 212
OY 275 ESQC 278

RESULT 5
ENTRY S20750 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C1)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety subtype ayw, patient C1
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS S20750
REFERENCE S20745
AUTHORS Lal, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mellis, A.; Porru, A.
#submission submitted to the EMBL Data Library, March 1992
#description Sequence analysis of HBV genomes isolated from patients with HBeAg negative chronic liver disease.
#accession S20750
#molecule_type DNA
#residues 1-212 #label LAI
#cross_references EMBL:X65258; NID:959434; PID:959436
#experimental_source subtype ayw, patient C1

GENETICS C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE 1-29
1-29 #domain signal sequence #status predicted #label SIG
30-212 #product core antigen #status predicted #label CAG
30-178 #product e antigen #status predicted #label EAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 147

Query Match 65.8%; Score 1373; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 9,36e-205;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALROAI 88
OY 95 SMDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSPHCSPHHTALROAI 154

Db 89 LCMGELMTLATVGVNLEDPASRDVSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 148
OY 155 LCMGELMTLATVGVNLEDPASRDVSVYNTNMGKFRQLMFIHISCLTFGRTVIEYL 214

Db 149 VAFGWIRTPPAYRPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
OY 215 VAFGWIRTPPAYRPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 274

Db 209 ESQC 212
OY 275 ESQC 278

RESULT 6
ENTRY S53270 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Licheri-2/87)
ALTERNATE_NAMES HBeC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Licheri-2/87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

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08-Sep-1997
ACCESSIONS      S53270
REFERENCE        S53112
#authors        Lai, M.E.; Mazzeoni, A.P.; Porru, A.; Balestrieri, A.
#submission     submitted to the EMBL Data Library, March 1995
#accession      S53270
##molecule_type DNA
##residues      1-183 ##label LAI
##cross-references EMBL:X85314; NID:g736201; PID:g736204
##experimental_source isolate patient Licheri-2/87
#note           due to a stop codon between the alternative initiators
                the e antigen precursor cannot be produced

GENETICS
#gene           C
CLASSIFICATION  #superfamily hepatitis B virus core antigen
KEYWORDS        core protein
SUMMARY         #length 183 #molecular-weight 21102 #checksum 2199

Query Match      65.6%: Score 1370; DB 2: Length 183;
Best Local Similarity 98.4%: Pred. No. 3,066-204;
Matches 180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDYKEFGATVELSLTSPDFSPVBDLDTASALYRALSEPHCSPHNTALROAIL 60
Qy 96 MDIDYKEFGATVELSLTSPDFSPVBDLDTASALYRALSEPHCSPHNTALROAIL 155
Qy 156 CWGELMTLATWGVNLDPASRDVSVYNTNMGLEKFRQLMFIISCLTFGRFVIEYLV 215
Db 61 CWGDLMTLATWGVNLDPASRDVSVYNTNMGLEKFRQLMFIISCLTFGRFVIEYLV 120
Qy 156 CWGELMTLATWGVNLDPASRDVSVYNTNMGLEKFRQLMFIISCLTFGRFVIEYLV 215
Db 121 SFGVIRIRPPAYRPPNAIILSLPTTYVRRGRPPRRRTSPRRRSQSRRRSQSRE 180
Qy 216 SFGVIRIRPPAYRPPNAIILSLPTTYVRRGRGSPRRRTSPRRRSQSRRRSQSRE 275
Db 181 SOC 183
Qy 276 SOC 278

RESULT          7
ENTRY           S53216 #type complete
TITLE           e antigen precursor / core antigen - hepatitis B virus
                (isolate patient Castag'3)
ALTERNATE_NAMES HBe antigen precursor / Hbc antigen; pre-C/C antigen
CONTAINS        core antigen; e antigen
ORGANISM        #formal_name hepatitis B virus; HBV
VARIETY          isolate patient Castag'3
DATE            08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                08-Sep-1997

ACCESSIONS      S53216
REFERENCE        S53112
#authors        Lai, M.E.; Mazzeoni, A.P.; Porru, A.; Balestrieri, A.
#submission     submitted to the EMBL Data Library, March 1995
#accession      S53216
##molecule_type DNA
##residues      1-212 ##label LAI
##cross-references EMBL:X85293; NID:g736124; PID:g736126
##experimental_source isolate patient Castag'3

GENETICS
#gene           C
CLASSIFICATION  #superfamily hepatitis B virus core antigen
KEYWORDS        alternative initiators; core protein
FEATURES
1-29            #domain signal sequence #status predicted #label SIG\
30-212          #product core antigen #status predicted #label CAG\
30-178          #product e antigen #status predicted #label EAG\
179-212        #domain carboxyl-terminal propeptide #link EAG #status
                predicted #label ECP
SUMMARY         #length 212 #molecular-weight 24363 #checksum 752

Query Match      65.6%: Score 1370; DB 2: Length 212;
Best Local Similarity 98.9%: Pred. No. 3,066-204;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

Db	29	GMDIDPYKEFGATVLLSFLSDSPFSRDLDDNASALYREALSEPCSHHTLRAI	88
Qy	95	SMDIDPYKEFGATVLLSFLSDSPFSRDLDDNASALYREALSEPCSHHTLRAI	154
Db	89	LCMGELMLTLATWGVNLEDPASRDLYSVYNTNMGLKFRQLMFIISCLTIGRETIVELYL	148
Qy	155	LCMGELMLTLATWGVNLEDPASRDLYSVYNTNMGLKFRQLMFIISCLTIGRETIVELYL	214
Db	149	VSGFWIRTPPAYRPNPAPILISTLEPTTVARRGRSSPRRRPSPPRRRSQSPPRRRSOSR	208
Qy	215	VSGFWIRTPPAYRPNPAPILISTLEPTTVARRGRSSPRRRPSPPRRRSQSPPRRRSOSR	274
Db	209	ESQC 212	
Qy	275	ESQC 278	
<hr/>			
RESULT	8		
ENTRY		S53272	#type complete
TITLE		e antigen precursor / core antigen - hepatitis B virus (isolate patient Licheiri-3'90)	
ALTERNATE_NAMES		HBe antigen precursor / Hbc antigen; pre-C/C antigen	
CONTAINS		core antigen; e antigen	
ORGANISM		#formal_name hepatitis B virus, HBV	
DATE		isolate patient Licheiri-3'90 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997	
ACCESSIONS		S53272	
REFERENCE		S53112	
#authors		Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.	
#submitter		submitted to the EMBL Data Library, March 1995	
#accession		S53272	
##molecule_type		DNA	
##residues		1-212 ##label LAI	
##cross-references		EMBL:X85315; NID:g736205; PID:g736207	
##experimental_source		isolate patient Licheiri-3'90	
GENETICS			
CLASSIFICATION	C	#superfamily hepatitis B virus core antigen	
KEYWORDS		alternative initiators; core protein	
FEATURE			
1-29		#domain signal sequence #status predicted #label SIG\	
30-212		#product core antigen #status predicted #label CAG\	
30-178		#product e antigen #status predicted #label EAG\	
179-212		#domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP	
SUMMARY		#length 212 #molecular_weight 24366 #checksum 446	
Query Match		65.6%; Score 1370; DB 2; Length 212;	
Best Local Similarity		98.9%; Pred. No. 3,06e-204;	
Matches 182; Conservative		1; Mismatches 1; Indels 0; Gaps 0	
Db	29	GMDIDPYKEFGATVLLSFLSDSPFSRDLDDNASALYREALSEPCSHHTLRAI	88
Qy	95	SMDIDPYKEFGATVLLSFLSDSPFSRDLDDNASALYREALSEPCSHHTLRAI	154
Db	89	LCMGELMLTLATWGVNLEDPASRDLYSVYNTNMGLKFRQLMFIISCLTIGRETIVELYL	148
Qy	155	LCMGELMLTLATWGVNLEDPASRDLYSVYNTNMGLKFRQLMFIISCLTIGRETIVELYL	214
Db	149	VSGFWIRTPPAYRPNPAPILISTLEPTTVARRGRSSPRRRPSPPRRRSQSPPRRRSOSR	208
Qy	215	VSGFWIRTPPAYRPNPAPILISTLEPTTVARRGRSSPRRRPSPPRRRSQSPPRRRSOSR	274
Db	209	ESQC 212	
Qy	275	ESQC 278	
<hr/>			
ENTRY	9	S53163	#type complete
TITLE		e antigen precursor / core antigen - hepatitis B virus	

ALTERNATE_NAMES (isolate patient Vitorina'92)
CONTAINS HBe antigen precursor / HBeC antigen: pre-C/C antigen
ORGANISM core antigen: e antigen
#formal_name hepatitis B virus, HBV
#variety isolate patient Vitorina'92
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53163
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Portu, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53163
#molecule_type DNA
#residues 1-212 #label LAI
##cross-references EMBL:X85256; NID:G736050; PID:G736052
##experimental_source isolate patient Vitorina'92

GENETICS C
#gene
CLASSIFICATION #superfamily hepatitis B virus core antigen
FEATURES
KEYWORDS alternative initiators: core protein
1-29
30-212 #domain signal sequence #status predicted #label SIG
179-212 #product e antigen #status predicted #label EAG
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24322 #checksum 842

Query Match 65.6%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 4.53e-204;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHNTALROAI 88
:|||||
QY 95 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHNTALROAI 154
:|||||

Db 89 LCGELMTLATWGVNEDPASRDLYSVYNTNGLKFRQLMWHISCLTFGRVTEYL 148
:|||||
QY 155 LCGELMTLATWGVNEDPASRDLYSVYNTNGLKFRQLMWHISCLTFGRVTEYL 214
:|||||

Db 149 VSEGVWIRTPPAYPPNAPILSTPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||
QY 215 VSEGVWIRTPPAYPPNAPILSTPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 274
:|||||

Db 209 ESQC 212
:|||||
QY 275 ESQC 278

RESULT 10
ENTRY S20746 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen: pre-C/C antigen
CONTAINS core antigen: e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety subtype ayw, patient C
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997

ACCESSIONS S20746
REFERENCE S20745
#authors Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.;
Portu, A.
#submission submitted to the EMBL Data Library, March 1992
#description Sequence analysis of HBV genomes isolated from patients with
HBsAg negative chronic liver disease.
#accession S20746
#molecule_type DNA
#residues 1-212 #label LAI
##cross-references EMBL:X65257; NID:G59429; PID:G59431
##experimental_source subtype ayw, patient C

GENETICS C
#gene

CLASSIFICATION #superfamily hepatitis B virus core antigen
FEATURES
KEYWORDS alternative initiators: core protein
1-29
30-212 #domain signal sequence #status predicted #label SIG
179-212 #product e antigen #status predicted #label EAG
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 506

Query Match 65.6%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.53e-204;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHNTALROAI 88
:|||||
QY 95 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHNTALROAI 154
:|||||

Db 89 LCGELMTLATWGVNEDPASRDLYSVYNTNGLKFRQLMWHISCLTFGRVTEYL 148
:|||||
QY 155 LCGELMTLATWGVNEDPASRDLYSVYNTNGLKFRQLMWHISCLTFGRVTEYL 214
:|||||

Db 149 VSEGVWIRTPPAYPPNAPILSTPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||
QY 215 VSEGVWIRTPPAYPPNAPILSTPETTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 274
:|||||

Db 209 ESQC 212
:|||||
QY 275 ESQC 278

RESULT 11
ENTRY S53225 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Chigline-2'86)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen: pre-C/C antigen
CONTAINS core antigen: e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Chigline-2'86
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53225
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Portu, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53225
#molecule_type DNA
#residues 1-212 #label LAI
##cross-references EMBL:X85296; NID:G736137; PID:G736139
##experimental_source isolate patient Chigline-2'86

GENETICS C
#gene
CLASSIFICATION #superfamily hepatitis B virus core antigen
FEATURES
KEYWORDS alternative initiators: core protein
1-29
30-212 #domain signal sequence #status predicted #label SIG
179-212 #product e antigen #status predicted #label EAG
#domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24308 #checksum 655

Query Match 65.6%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.53e-204;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHNTALROAI 88
:|||||
QY 95 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHNTALROAI 154
:|||||

Db 89 LCGELMTLATWGVNEDPASRDLYSVYNTNGLKFRQLMWHISCLTFGRVTEYL 148
:|||||
QY 155 LCGELMTLATWGVNEDPASRDLYSVYNTNGLKFRQLMWHISCLTFGRVTEYL 214
:|||||

Query Match	Score	DB 2	Length	212
65.4%	Score 1366;	DB 2;	Length 212;	
Best Local Similarity 97.8%;	Pred. No. 1,48e-203;			
Matches 180;	Conservative 3;	Mismatches 1;	Indels 0;	Gaps 0
<p> REFERENCE #authors Lali, M.E.; Mazzoleni, A.P.; Portu, A.; Balestrieri, A. #submission Submitted to the EMBL Data Library, March 1995 #accession S53223 ##molecule_type DNA ##residues 1-212 ##label LAI ##cross-references EMBL:X85316; NID:g736134; PID:g736136 ##experimental_source isolate patient Chigline-1/85 </p> <p> GENETICS #gene #superfamily hepatitis B virus core antigen CLASSIFICATION alternative initiators; core protein KEYWORDS FEATURE 1-29 30-212 30-178 179-212 </p> <p> #domain signal sequence #status predicted #label SIG\ #product core antigen #status predicted #label CAC\ #product core antigen #status predicted #label CAC\ #domain carboxyl-terminal propetide #link EAG #status predicted #label ECP </p> <p> #length 212 #molecular-weight 24364 #checksum 1123 </p>				
<p> SUMMARY #length 212 #molecular-weight 24364 #checksum 1123 </p>				
Query Match	65.4%	Score 1366;	DB 2;	Length 212;
Best Local Similarity 97.8%;	Pred. No. 1,48e-203;			
Matches 180;	Conservative 3;	Mismatches 1;	Indels 0;	Gaps 0
<p> REFERENCE #authors Lali, M.E.; Mazzoleni, A.P.; Portu, A.; Balestrieri, A. #submission Submitted to the EMBL Data Library, March 1995 #accession S53224 ##molecule_type DNA ##residues 1-212 ##label LAI ##cross-references EMBL:X85316; NID:g736208; PID:g736210 ##experimental_source isolate patient Chigline-1/85 </p> <p> GENETICS #gene #superfamily hepatitis B virus core antigen CLASSIFICATION alternative initiators; core protein KEYWORDS FEATURE 1-29 30-212 30-178 179-212 </p> <p> #domain signal sequence #status predicted #label SIG\ #product core antigen #status predicted #label CAC\ #product core antigen #status predicted #label CAC\ #domain carboxyl-terminal propetide #link EAG #status predicted #label ECP </p> <p> #length 212 #molecular-weight 24376 #checksum 390 </p>				
Query Match	65.4%	Score 1366;	DB 2;	Length 212;

Best Local Similarity 98.98; Pred. No. 1,48e-203;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEGATVEELSLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
QY 95 SMDIDPYKEGATVEELSLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 154
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTFGRETVEIYL 148
QY 155 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTFGRETVEIYL 214
Db 149 VSGVWIRTPPAYRPPNAPILILPETTVYRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 215 VSGVWIRTPPAYRPPNAPILILPETTVYRRGRSPRRRTSPRRRSQSPRRRSQSR 274
Db 209 ESOC 212
QY 275 ESOC 278

RESULT 15
ENTRY S53169 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Muresu'89)
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Muresu'89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53169
REFERENCE S53112
#authors Lai, M.E.; Mazzeoni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53169
##molecule_type DNA
##residues 1-183 #label LAI
##cross_references EMBL:X85275; NID:q736057; PID:q736060
##experimental_source isolate patient Muresu'89
##note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
SUMMARY #length 183 #molecular_weight 21088 #checksum 1849

Query Match 65.38; Score 1364; DB 2; Length 183;
Best Local Similarity 98.48; Pred. No. 3.26e-203;
Matches 180; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDIDPYKEGATVEELSLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 60
QY 96 MDIDPYKEGATVEELSLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 155
Db 61 CMCGLMTLATWGANLEDPASRDLYSVYNTNMGKFRQLMFHISCLTFGRETVEIYL 120
QY 156 CMCGLMTLATWGANLEDPASRDLYSVYNTNMGKFRQLMFHISCLTFGRETVEIYL 215
Db 121 SFGVWIRTPPAYRPPNAPILILPETTVYRRGRSPRRRTSPRRRSQSPRRRSQSR 180
QY 216 SFGVWIRTPPAYRPPNAPILILPETTVYRRGRSPRRRTSPRRRSQSPRRRSQSR 275
Db 181 SQC 183
QY 276 SQC 278

Search completed: Thu Dec 16 13:24:56 1999
Job time : 57 secs.

W O R L D
(TM)

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Mpsrch-pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 13:25:14 1999; MasPar time 9.63 seconds
Tabular output not generated. 816.384 Million cell updates/sec

Title: >US3869-29-38183
Description: (1-278) from us3869-29-38183.pep
Perfect Score: 2088
Sequence: 1 MDIDPYKEFGATVELLSFLP.....RRRRSQSPRRRSQSRSSQC 278

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 48.215; Variance 102.691; scale 0.470

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1374	65.8	183	1	CORA_HPBVA CORE ANTIGEN.	9.32e-236
2	1358	65.0	211	1	CORA_HPBVA CORE ANTIGEN.	1.32e-232
3	1349	64.6	183	1	CORA_HPBVA CORE ANTIGEN.	7.85e-231
4	1336	64.0	183	1	CORA_HPBVA CORE ANTIGEN.	2.85e-228
5	1334	63.9	183	1	CORA_HPBVA CORE ANTIGEN.	7.06e-228
6	1332	63.3	183	1	CORA_HPBVA CORE ANTIGEN.	1.62e-225
7	1331	63.3	183	1	CORA_HPBVA CORE ANTIGEN.	2.56e-225
8	1314	62.9	195	1	CORA_HPBVA CORE ANTIGEN.	6.10e-224
9	1313	62.9	212	1	CORA_HPBVA CORE ANTIGEN.	9.59e-224
10	1308	62.6	183	1	CORA_HPBVA CORE ANTIGEN.	9.24e-223
11	1305	62.5	185	1	CORA_HPBVA CORE ANTIGEN.	3.60e-222
12	1304	62.5	214	1	CORA_HPBVA CORE ANTIGEN.	5.66e-222
13	938	44.9	188	1	CORA_HPBVA CORE ANTIGEN.	1.96e-150
14	933	44.7	187	1	CORA_HPBVA CORE ANTIGEN.	1.83e-149
15	934	44.7	217	1	CORA_HPBVA CORE ANTIGEN.	1.17e-149
16	208	10.0	493	1	CETP_HUMAN CHOLESTERYL ESTER TRAN	1.19e-15
17	208	10.0	493	1	CETP_HUMAN CHOLESTERYL ESTER TRAN	1.19e-15
18	205	9.8	289	1	CETP_HUMAN CHOLESTERYL ESTER TRAN	3.58e-15
19	200	9.6	305	1	CORA_HPBVA CORE ANTIGEN.	2.21e-14
20	200	9.6	305	1	CORA_HPBVA CORE ANTIGEN.	2.21e-14
21	200	9.6	305	1	CORA_HPBVA CORE ANTIGEN.	2.21e-14
22	200	9.6	305	1	CORA_HPBVA CORE ANTIGEN.	2.21e-14
23	200	9.6	305	1	CORA_HPBVA CORE ANTIGEN.	2.21e-14

RESULT	ID	Score	Query Match	Length	ID	Description	Pred. No.
24	171	8.2	497	1	CETP_RABIT CHOLESTERYL ESTER TRAN	6.42e-10	
25	158	7.6	196	1	SPR2_CAEEL PUTATIVE SPLICING FACT	5.35e-08	
26	148	7.1	208	1	YSX2_CAEEL HYPOPHYSAL 24.0 KD P	1.46e-06	
27	136	6.5	78	1	PR12_SEPOF SPERMATID-SPECIFIC PRO	6.81e-05	
28	131	6.3	61	1	SPR1_MACCU SPERMATID-SPECIFIC PRO	3.22e-04	
29	130	6.2	77	1	PR12_SEPOF SPERMATID-SPECIFIC PRO	4.39e-04	
30	125	6.0	60	1	SPR1_MACCU SPERMATID-SPECIFIC PRO	2.01e-03	
31	125	6.0	61	1	SPR1_MACCU SPERMATID-SPECIFIC PRO	2.01e-03	
32	126	6.0	498	1	VE2_HPV08 REGULATORY PROTEIN E2	1.48e-03	
33	126	6.0	1523	1	SON_HUMAN SON PROTEIN (SON3)	1.48e-03	
34	124	5.9	57	1	HSP1_DIDNA SPERMATID-SPECIFIC PRO	2.71e-03	
35	121	5.8	61	1	HSP1_CHICK SPERMATID-SPECIFIC PRO	6.61e-03	
36	122	5.8	91	1	PH1_MYTED SPERMATID-SPECIFIC PRO	4.92e-03	
37	122	5.8	132	1	PR12_SEPOF SPERMATID-SPECIFIC PRO	4.92e-03	
38	121	5.8	739	1	DD13_CAEEL PUTATIVE PRE-MRNA SPLI	6.61e-03	
39	121	5.8	843	1	CYP1_BRUMA PEPTIDYLPROLYL ISOMERA	6.61e-03	
40	119	5.7	50	1	HSP1_MART SPERMATID-SPECIFIC PRO	1.19e-02	
41	119	5.7	50	1	HSP1_MART SPERMATID-SPECIFIC PRO	1.19e-02	
42	118	5.7	238	1	SPR7_HUMAN SPLICING FACTOR, ARGIN	1.59e-02	
43	118	5.7	576	1	CAT4_RHOCA PEROXIDASE / CATALASE	1.59e-02	
44	115	5.5	102	1	HSP2_MACCU SPERMATID-SPECIFIC PRO	3.79e-02	
45	115	5.5	104	1	HSP2_CALVA SPERMATID-SPECIFIC PRO	3.79e-02	

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description	Pred. No.
1	CORA_HPBVA	65.8	183	1	CORA_HPBVA	CORE ANTIGEN.	9.32e-236
2	1374	65.8	183	1	CORA_HPBVA	CORE ANTIGEN.	9.32e-236
3	1358	65.0	211	1	CORA_HPBVA	CORE ANTIGEN.	1.32e-232
4	1349	64.6	183	1	CORA_HPBVA	CORE ANTIGEN.	7.85e-231
5	1336	64.0	183	1	CORA_HPBVA	CORE ANTIGEN.	2.85e-228
6	1334	63.9	183	1	CORA_HPBVA	CORE ANTIGEN.	7.06e-228
7	1332	63.3	183	1	CORA_HPBVA	CORE ANTIGEN.	1.62e-225
8	1331	63.3	183	1	CORA_HPBVA	CORE ANTIGEN.	2.56e-225
9	1314	62.9	195	1	CORA_HPBVA	CORE ANTIGEN.	6.10e-224
10	1313	62.9	212	1	CORA_HPBVA	CORE ANTIGEN.	9.59e-224
11	1308	62.6	183	1	CORA_HPBVA	CORE ANTIGEN.	9.24e-223
12	1305	62.5	185	1	CORA_HPBVA	CORE ANTIGEN.	3.60e-222
13	1304	62.5	214	1	CORA_HPBVA	CORE ANTIGEN.	5.66e-222
14	938	44.9	188	1	CORA_HPBVA	CORE ANTIGEN.	1.96e-150
15	933	44.7	187	1	CORA_HPBVA	CORE ANTIGEN.	1.83e-149
16	208	10.0	493	1	CETP_HUMAN	CHOLESTERYL ESTER TRAN	1.19e-15
17	208	10.0	493	1	CETP_HUMAN	CHOLESTERYL ESTER TRAN	1.19e-15
18	205	9.8	289	1	CETP_HUMAN	CHOLESTERYL ESTER TRAN	3.58e-15
19	200	9.6	305	1	CORA_HPBVA	CORE ANTIGEN.	2.21e-14
20	200	9.6	305	1	CORA_HPBVA	CORE ANTIGEN.	2.21e-14
21	200	9.6	305	1	CORA_HPBVA	CORE ANTIGEN.	2.21e-14
22	200	9.6	305	1	CORA_HPBVA	CORE ANTIGEN.	2.21e-14
23	200	9.6	305	1	CORA_HPBVA	CORE ANTIGEN.	2.21e-14

Query Match: 65.8%; Score 1374; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.32e-236;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAIL 60
 QY 96 MDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAIL 155
 Db 61 CWGELMTLATWGVNLEDPASRDVLVS YVNTNMGKFRQLMFIHISCLTFGRETVEYLV 120
 QY 156 CWGELMTLATWGVNLEDPASRDVLVS YVNTNMGKFRQLMFIHISCLTFGRETVEYLV 215
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
 QY 216 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 275
 Db 181 SOC 183
 QY 276 SOC 278

RESULT 2
 ID CORA_HPBYA STANDARD; PRT; 211 AA.
 AC P24023;
 DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DE CORE ANTIGEN.
 CC
 GN HEPATITIS B VIRUS (STRAIN ALPHA1).
 OS VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90266476.
 RA TONG S., LI J., VITVITSKI L., TREPO C.;
 RT "Active hepatitis B virus replication in the presence of anti-HBe is
 associated with viral variants containing an inactive pre-C region.";
 RL VIROLOGY 176:596-603(1990).

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DR EMBL: M32138; G495034; ALT_SEQ.
 DR PIR: A34773; NKVLAL.
 DR PFAM: PF00906; Hepatitis_core; 1.
 KW CORE PROTEIN; REPEAT.
 FT REPEAT 183 190
 FT REPEAT 198 206
 SQ SEQUENCE 211 AA; 24208 MW; 0924CE5E CRC32;

Query Match 65.0%; Score 1358; DB 1; Length 211;
 Best Local Similarity 95.2%; Pred. No. 1,32e-232;
 Matches 179; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 24 LGWMDMDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 83
 QY 91 LQSLMSMDIDPKKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 150
 Db 84 ROAILCWGDLTLTSTWGVNLEDPSTSDVLVS YVNTNMGKFRQLMFIHISCLTFGRETVEYLV 143
 QY 151 ROAILCWGDLTLTSTWGVNLEDPSTSDVLVS YVNTNMGKFRQLMFIHISCLTFGRETVEYLV 210
 Db 144 IEYLVSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRR 203
 QY 211 IEYLVSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRR 270
 Db 204 TQSRSSOC 211
 QY 271 TQSRSSOC 278

RESULT 3
 ID CORA_HPBYZ STANDARD; PRT; 183 AA.
 AC P03147;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN
 CC
 OS HEPATITIS B VIRUS (SUBTYPE ADYN).
 OS VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 81012115.
 RA PASER M., GOTO T., GILBERT W., ZINK B., SCHALLER H., MCKAY P.,
 RA LEADBETTER G., MURRAY K.;
 RT "Hepatitis B virus genes and their expression in E. coli.";
 RL NATURE 282:575-579(1979).

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DR EMBL: J02202; G329638; -
 DR EMBL: A08967; G411874; -
 DR PIR: B93217; NKVLAL.
 DR PFAM: PF00906; Hepatitis_core; 1.
 KW CORE PROTEIN; REPEAT.
 FT REPEAT 162 169
 FT REPEAT 170 177
 SQ SEQUENCE 183 AA; 21042 MW; 6EA6B674 CRC32;

Query Match 64.6%; Score 1349; DB 1; Length 183;
 Best Local Similarity 96.7%; Pred. No. 7.85e-231;
 Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAIL 60
 QY 96 MDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAIL 155
 Db 61 CWGELMTLATWGVNLEDPASRDVLVS YVNTNMGKFRQLMFIHISCLTFGRETVEYLV 120
 QY 156 CWGELMTLATWGVNLEDPASRDVLVS YVNTNMGKFRQLMFIHISCLTFGRETVEYLV 215
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
 QY 216 SFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 275
 Db 181 SOC 183
 QY 276 SOC 278

RESULT 4
 ID CORA_HPBYO STANDARD; PRT; 183 AA.
 AC P17392;
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 CC
 OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN OKINAWA/POOW282).
 OS VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89010694.
 RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASUROSEWIGNO R.I., IMAI M.,
 RA MIYAKAWA Y., MATSUMI M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:
 comparison of surface antigen subtypes.";

RL J. GEN. VIROL. 69:2575-2583(1988).
 CC -----
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 CC -----
 DR EMBL: D00330; -; NOT_ANNOTATED_CDS.
 DR PIR: B28925; NKVLJ2.
 DR PIR: B28925; Hepatitis_core: 1.
 KW CORE PROTEIN; REPEAT.
 FT REPEAT 162 169
 FT REPEAT 170 177
 SQ SEQUENCE 183 AA; 21081 MW; 115B9E3 CRC32;
 Query Match 64.0%; Score 1336; DB 1; Length 183;
 Best Local Similarity 96.2%; Pred. No. 2.85e-228;
 Matches 176; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MDIDPKFEGASVELSLSPDFFPSVRLDLDTSALYREALSEPHHIALROAIL 60
 |||||||
 Qy 96 MDIDPKFEGATVELSLSPDFFPSVRLDLDTSALYREALSEPHHIALROAIL 155
 |||||||
 Db 61 CMGELMTATWGSNLEDPASRELVSYNVMGKIRQLMFHISCLTFGREYIELV 120
 |||||||
 Qy 156 CMGELMTATWGSNLEDPASRDVSVYNTMGKIRQLMFHISCLTFGREYIELV 215
 |||||||
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETVVRGRGSPRRRTSPRRRSQSPRRRSQRE 180
 |||||||
 Qy 216 SFGWIRTPPAYRPPNAPILSTLPETVVRGRGSPRRRTSPRRRSQSPRRRSQRE 275
 |||||||
 Db 181 SOC 183
 ||||
 Qy 276 SOC 278
 ||||
 RESULT 5
 ID CORA_HPBVA STANDARD; PRT: 183 AA.
 AC P03150; P03151;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN C
 OS HEPATITIS B VIRUS (SUBTYPE ADP), HEPATITIS B VIRUS (SUBTYPE ADP4),
 OS AND HEPATITIS B VIRUS (SUBTYPE ADP / STRAIN INDONESIA/PIDM420).
 OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ADR:
 RX MEDLINE: 83168919.
 RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
 RT "The complete nucleotide sequences of the cloned hepatitis B virus
 RT DNA: subtype adr and adw.";
 RL NUCLEIC ACIDS RES. 11:1747-1757(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ADR4;
 RX MEDLINE: 83246570.
 RA FUJIVARA A., MIYANOYARA A., NOZAKI C., YONEYAMA T., OHTOMO N.,
 RA MATSUBARA K.;
 RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
 RT adr.";
 RL NUCLEIC ACIDS RES. 11:4601-4610(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ADM;
 RX MEDLINE: 89010694.
 RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
 RA MIYAKAWA Y., MAYUMI M.;

RT "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. GEN. VIROL. 69:2575-2583(1988).
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 CC -----
 DR EMBL: D00330; -; NOT_ANNOTATED_CDS.
 DR PIR: B28925; NKVLJ2.
 DR PIR: B28925; Hepatitis_core: 1.
 KW CORE PROTEIN; REPEAT.
 FT REPEAT 162 169
 FT REPEAT 170 177
 SQ SEQUENCE 183 AA; 21095 MW; D2E185B9 CRC32;
 Query Match 63.9%; Score 1334; DB 1; Length 183;
 Best Local Similarity 95.6%; Pred. No. 7.06e-228;
 Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 Db 1 MDIDPKFEGASVELSLSPDFFPSVRLDLDTSALYREALSEPHHIALROAIL 60
 |||||||
 Qy 96 MDIDPKFEGATVELSLSPDFFPSVRLDLDTSALYREALSEPHHIALROAIL 155
 |||||||
 Db 61 CMGELMTATWGSNLEDPASRELVSYNVMGKIRQLMFHISCLTFGREYIELV 120
 |||||||
 Qy 156 CMGELMTATWGSNLEDPASRDVSVYNTMGKIRQLMFHISCLTFGREYIELV 215
 |||||||
 Db 121 SFGWIRTPPAYRPPNAPILSTLPETVVRGRGSPRRRTSPRRRSQSPRRRSQRE 180
 |||||||
 Qy 216 SFGWIRTPPAYRPPNAPILSTLPETVVRGRGSPRRRTSPRRRSQSPRRRSQRE 275
 |||||||
 Db 181 SOC 183
 ||||
 Qy 276 SOC 278
 ||||
 RESULT 6
 ID CORA_HPBVA STANDARD; PRT: 183 AA.
 AC P17391;
 DT 01-AUG-1990 (REL. 15, CREATED)
 DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
 DE CORE ANTIGEN.
 GN C
 OS HEPATITIS B VIRUS (SUBTYPE ADP / STRAIN JAPAN/PJDM233).
 OS VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ADR:
 RX MEDLINE: 89010694.
 RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
 RA MIYAKAWA Y., MAYUMI M.;
 RT "Typing hepatitis B virus by homology in nucleotide sequence:
 RT comparison of surface antigen subtypes.";
 RL J. GEN. VIROL. 69:2575-2583(1988).
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 CC -----
 DR EMBL: D00330; -; NOT_ANNOTATED_CDS.
 DR PIR: A28925; NKVLJ1.

DR PFAM: PF00906; Hepatitis-core: 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21224 MW; F6B348B6 CRC32;
Query Match 63.3%; Score 1322; DB 1; Length 183;
Best Local Similarity 96.2%; Pred. No. 1,62e-225;
Matches 176; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
|||
QY 96 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 155
|||
Db 61 CWGELMTLATVGNLDDPASRDLYVNVNTNMGKIRQLMFMHISCLTFEGRETVLEYLV 120
|||
QY 156 CWGELMTLATVGNLDDPASRDLYVNVNTNMGKIRQLMFMHISCLTFEGRETVLEYLV 215
|||
Db 121 SFGWITPPAYRPNPAPILSTPETVYVRRGRSPRRRTSPRRRSQSPRRRSQSPRE 180
|||
QY 216 SFGWITPPAYRPNPAPILSTPETVYVRRGRSPRRRTSPRRRSQSPRRRSQSPRE 275
|||
Db 181 SOC 183
|||
QY 276 SOC 278
|||

RESULT 7
ID CORA_HPBVT STANDARD; PRT; 185 AA.
AC P03149;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83168919.
RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA; subtype adr and adw."
RL NUCLEIC ACIDS RES. 11:1747-1757(1983).
CC
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CC
CC EMBL: V00866; NOT_ANNOTATED_CDS.
DR PIR: C93460; NRYL46.
DR PFAM: PF00906; Hepatitis-core: 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 164 171
FT REPEAT 172 179
SQ SEQUENCE 185 AA; 21394 MW; 791E0381 CRC32;

Query Match 63.3%; Score 1321; DB 1; Length 185;
Best Local Similarity 96.2%; Pred. No. 2,56e-225;
Matches 178; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Db 1 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
|||
QY 96 MDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAIL 155
|||
Db 61 CWGELMTLATVGNLDDPASRDLYVNVNTNMGKIRQLMFMHISCLTFEGRETVLEYLV 120
|||
QY 156 CWGELMTLATVGNLDDPASRDLYVNVNTNMGKIRQLMFMHISCLTFEGRETVLEYLV 215
|||

Db 121 SFGWITPPAYRPNPAPILSTPETVYVRRGRSPRRRTSPRRRSQSPRRRSQSPRE 180
|||
QY 216 SFGWITPPAYRPNPAPILSTPETVYVRRGRSPRRRTSPRRRSQSPRRRSQSPRE 273
|||
Db 181 RESOC 185
|||
QY 274 RESOC 278
|||

RESULT 8
ID CORA_HPBVT STANDARD; PRT; 195 AA.
AC P29178;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW2 VARIANT SF).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90169850.
RA BHAT R.A., ULRICH P.P., VYAS G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
RT a persistently infected homosexual man."
RL HEPATOLOGY 11:271-276(1990).
DR PIR: A37182; NRYL43.
DR PFAM: PF00906; Hepatitis-core: 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 174 181
FT REPEAT 182 188
SQ SEQUENCE 195 AA; 22461 MW; AF3DB5F3 CRC32;

Query Match 62.9%; Score 1314; DB 1; Length 195;
Best Local Similarity 93.5%; Pred. No. 6,10e-224;
Matches 173; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 11 FGIDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROA 70
|||
QY 94 LSMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROA 153
|||
Db 71 ILVWEVMTLATVGNLDDPASRDLYVNVNTNMGKIRQLMFMHISCLTFEGRETVLEY 130
|||
QY 154 ILVWEVMTLATVGNLDDPASRDLYVNVNTNMGKIRQLMFMHISCLTFEGRETVLEY 213
|||
Db 131 LVSPGWITPPAYRPNPAPILSTPETVYVRRGRSPRRRTSPRRRSQSPRRRSQSPRE 190
|||
QY 214 LVSPGWITPPAYRPNPAPILSTPETVYVRRGRSPRRRTSPRRRSQSPRRRSQSPRE 273
|||
Db 191 RESOC 195
|||
QY 274 RESOC 278
|||

RESULT 9
ID CORA_HPBVT STANDARD; PRT; 212 AA.
AC 005495;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE W4B).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93346870.
RA NAKUMANN H., SCHAEFER S., YOSHIDA C.F.T., GASPAR A.M.C., REPP R.,
RA GERLICH W.H.;
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
RT that expresses HBV surface antigen subtype adw4."
RL J. GEN. VIROL. 74:1627-1632(1993).
CC


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OS HEPATITIS B VIRUS (SUBTYPE ADM / STRAIN 991).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA KOEHEL H.G., SCHUELER A., LOTTWANN S., THOMSEN R.;
RC SUBMITTED (FEB-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
RL -----
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CC -----
DR EMBL: X51970; G60433; -
DR PIR: S10381; NKVLKS; -
DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 786CD048 CRC32;

Query Match
Best Local Similarity 95.2%; Pred. No. 5,66e-222;
Matches 177; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Db 29 GMDIDPKKEGATVELLSFSPDFPVRDLDTASALYREALSPHCSPHHTALROAI 88
QY 95 SMIDPKKEGATVELLSFSPDFPVRDLDTASALYREALSPHCSPHHTALROAI 154
Db 89 LCMGELMTLATWGNLDPASRDLYVYNTNGKIRQLMFRISYLTGEGTVEYL 148
QY 155 LCMGELMTLATWGNLDPASRDLYVYNTNGKIRQLMFRISYLTGEGTVEYL 214
Db 149 VSGVWIRTPAPYRPPNAPILSTLPETTVRRDRGSPRRRSPRRRSQ 208
QY 215 VSGVWIRTPAPYRPPNAPILSTLPETTVRRR--GRSPRRTPSPRRRSQSPRRRR 272
Db 209 SRESQC 214
QY 273 SRESQC 278

RESULT 13
ID CORA_MHV1 STANDARD; PRT; 188 AA.
AC P03152;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 1 (MHV 1),
OS WOODCHUCK HEPATITIS VIRUS 7 (MHV 7),
OS WOODCHUCK HEPATITIS VIRUS 59 (MHV 59), AND
OS WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE) (MHV 8).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA GALBERT F., CHEN T.N., MANDART E.;
RC SPECIES=WOODCHUCK HEPATITIS VIRUS 1;
RX MEDLINE: 82216969;
RA COHEN J.I., MILLER R.H., ROSENBLUM B., DENNISTON K., GERIN J.L.,
RA PURCELL R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RT shows conservation of the genome.";

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RL VIROLOGY 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE);
RX MEDLINE: 89184524;
RA GIRONES R., COTE P.J., HORNBUCKLE W.E., TENNANT B.C., GERIN J.L.,
RA PURCELL R.H., MILLER R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RT hepatitis virus that is infectious in the natural host.";
RL PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
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CC -----
DR EMBL: J02442; G336129; -
DR EMBL: M18752; G336140; -
DR EMBL: M19183; G336145; -
DR EMBL: J04514; G336149; -
DR PIR: A05713; NKVLC; -
DR PIR: C32397; NKVLC; -
DR PIR: C32397; NKVLC; -
DR PIR: C32397; NKVLC; -
DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; A667DB27 CRC32;

Query Match
Best Local Similarity 67.0%; Score 938; DB 1; Length 188;
Matches 126; Conservative 25; Mismatches 32; Indels 5; Gaps 1;

Db 1 MDIDPKKEGSSYQLNPLDFFPDNLAVDTATAYEEDLTGRHCSPHHTALROAI 60
QY 96 MDIDPKKEGATVELLSFSPDFPVRDLDTASALYREALSPHCSPHHTALROAI 155
Db 61 CWDELTKLIAMSSNITSQVRIIYNVNDTWGLKVRQSLMFLHSCLTFGHTQVEFLV 120
QY 156 CWGELMTLATWGNLDPASRDLYVYNTNGKIRQLMFRISYLTGEGTVEYL 215
Db 121 SFGVWIRTPAPYRPPNAPILSTLPETTVRRRGARASPPRRTPSPRRRSQSPRRRR 180
QY 216 SFGVWIRTPAPYRPPNAPILSTLPETTVRRRG-----RSPRRTPSPRRRSQSPRRRR 270
Db 181 SQSPSANC 188
QY 271 SQSPSANC 278

RESULT 14
ID CORA_MHV8 STANDARD; PRT; 187 AA.
AC P06433;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 8 (MHV 8).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA KODAWA K., OGASAWARA N., YOSHIKAWA H., MORAYAMI S.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT evolutionary relationship between hepadnaviruses.";
RL J. VIROL. 56:978-986(1985).
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Query Match 65.9%; Score 1375; DB 14; Length 212;
Best Local Similarity 99.5%; Pred. No. 3.17e-226;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
:|||||
QY 95 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 154
:|||||
Db 89 LCMGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLMFHISCLTFGRETIVIELY 148
:|||||
QY 155 LCMGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLMFHISCLTFGRETIVIELY 214
:|||||
Db 149 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
:|||||
QY 215 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 274
:|||||
Db 209 ESQC 212
:|||||
QY 275 ESQC 278

RESULT 2 PRELIMINARY: PRT: 183 AA.

ID 089437
AC 089437;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X. PREC AND C GENES (CASTA 2).
GN CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RC STRAIN-PATIENT CASTA-2'87;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85289; G736113; -;
DR EMBL: X80925; E198085; -;
DR PRAM: PF00906; Hepatitis_core: 1;
SQ SEQUENCE 183 AA; 21102 MW; 0C504D47 CRC32;

Query Match 65.8%; Score 1373; DB 14; Length 183;
Best Local Similarity 99.5%; Pred. No. 7.57e-226;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
:|||||
QY 96 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 155
:|||||
Db 61 CMGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLMFHISCLTFGRETIVIELY 120
:|||||
QY 156 CMGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLMFHISCLTFGRETIVIELY 215
:|||||
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
:|||||
QY 216 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 275
:|||||
Db 181 SOC 183
:|||||
QY 276 SOC 278

RESULT 3

ID 068008 PRELIMINARY: PRT: 183 AA.

AC 068008;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X. PREC AND C GENES (FERRACOTTI 1).
GN CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT FERRACOTTI-1'89;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85284; G736098; -;
DR PRAM: PF00906; Hepatitis_core: 1;
SQ SEQUENCE 183 AA; 21102 MW; BB9A7FB3 CRC32;

Query Match 65.8%; Score 1373; DB 14; Length 183;
Best Local Similarity 99.5%; Pred. No. 7.57e-226;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
:|||||
QY 96 MDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 155
:|||||
Db 61 CMGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLMFHISCLTFGRETIVIELY 120
:|||||
QY 156 CMGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLMFHISCLTFGRETIVIELY 215
:|||||
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
:|||||
QY 216 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 275
:|||||
Db 181 SOC 183
:|||||
QY 276 SOC 278

RESULT 4 PRELIMINARY: PRT: 212 AA.

ID 068020
AC 068020;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTAG-1'85;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85291; G736119; -;
DR PRAM: PF00906; Hepatitis_core: 1;
SQ SEQUENCE 212 AA; 24336 MW; E0E4C243 CRC32;

Query Match 65.8%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 4.90e-226;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
:|||||
QY 95 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 154
:|||||
Db 89 LCMGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLMFHISCLTFGRETIVIELY 148
:|||||
QY 155 LCMGELMTLATWGVNLEDPASRDVLVSYVNTNMGKFRQLMFHISCLTFGRETIVIELY 214
:|||||
Db 149 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
:|||||
QY 215 VSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 274
:|||||

Db 209 ESOC 212
|||
QY 275 ESOC 278

RESULT 5
ID 089597 PRELIMINARY; PRT; 212 AA.
AC 089597;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HEPATITIS B VIRUS.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUB-TYPE AYW;
RX MEDLINE: 94079539.
RA PREISLER-ADAMS S., SCHLAYER M.J., PETERS T., HETTLER F., GEROK W.,
RA RASENACK J.;
RT "Sequence analysis of hepatitis B virus DNA in immunologically
RT negative infection."
RL ARCH. VIROL. 133:385-396(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X72702; G288930; -
DR EMBL: X80925; E198084; -
DR PFAM: PF00906; Hepatitis core: 1
SQ SEQUENCE 212 AA; 24336 MW; 575D20BF CRC32;

Query Match 65.8%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 4.90e-226;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKREGATVELLSFLPSDFPSVRLDITASALYREALSPHCSPHHTALROAI 88
:|||||
QY 95 SMDIDPKREGATVELLSFLPSDFPSVRLDITASALYREALSPHCSPHHTALROAI 154

Db 89 LCMGELMTLATWGVNLEDPAASRDVSVYNTNGLKFRQLMWHISCLTFGRTVIEYL 148
:|||||
QY 155 LCMGELMTLATWGVNLEDPAASRDVSVYNTNGLKFRQLMWHISCLTFGRTVIEYL 214

Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||
QY 215 VSEFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSR 274

Db 209 ESOC 212
|||
QY 275 ESOC 278

RESULT 6
ID 067876 PRELIMINARY; PRT; 212 AA.
AC 067876;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE C/C ORF.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CI, HBV SUBTYPE AYW;
LAI M.E., MAZOLENTI A.P., BALESTRIERI A., MELIS A., PORRU A.;

RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65258; G59436; -
DR PFAM: PF00906; Hepatitis core: 1
SQ SEQUENCE 212 AA; 24346 MW; 6ED741BE CRC32;

Query Match 65.8%; Score 1373; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 7.57e-226;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKREGATVELLSFLPSDFPSVRLDITASALYREALSPHCSPHHTALROAI 88
:|||||
QY 95 SMDIDPKREGATVELLSFLPSDFPSVRLDITASALYREALSPHCSPHHTALROAI 154

Db 89 LCMGELMTLATWGVNLEDPAASRDVSVYNTNGLKFRQLMWHISCLTFGRTVIEYL 148
:|||||
QY 155 LCMGELMTLATWGVNLEDPAASRDVSVYNTNGLKFRQLMWHISCLTFGRTVIEYL 214

Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||
QY 215 VSEFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSR 274

Db 209 ESOC 212
|||
QY 275 ESOC 278

RESULT 7
ID 011884 PRELIMINARY; PRT; 212 AA.
AC 011884;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN PRECURSOR.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA RAO B.S., CASEY J.L., RINAUDO J.S., KORBA B.E.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U95551; G2182120; -
DR PFAM: PF00906; Hepatitis core: 1
SQ SEQUENCE 212 AA; 24360 MW; 73AC92DB CRC32;

Query Match 65.7%; Score 1372; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.17e-225;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKREGATVELLSFLPSDFPSVRLDITASALYREALSPHCSPHHTALROAI 88
:|||||
QY 95 SMDIDPKREGATVELLSFLPSDFPSVRLDITASALYREALSPHCSPHHTALROAI 154

Db 89 LCMGELMTLATWGVNLEDPAASRDVSVYNTNGLKFRQLMWHISCLTFGRTVIEYL 148
:|||||
QY 155 LCMGELMTLATWGVNLEDPAASRDVSVYNTNGLKFRQLMWHISCLTFGRTVIEYL 214

Db 149 VSEFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||
QY 215 VSEFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSR 274

Db 209 EPIC 212
|||
QY 275 ESOC 278

RESULT 8
ID 068066 PRELIMINARY; PRT; 183 AA.
AC 068066;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (LICHERI 2).
GN CORE.
OS HEPATITIS B VIRUS.

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OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LICHERI-2'87;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85314; G736204; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 183 AA; 21102 MW; 6F38A3B CRC32;

Query Match
Best Local Similarity 98.4%; Score 1370; DB 14; Length 183;
Matches 180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAI 60
   |||||||
QY 96 MDIDPKKFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAI 155
   |||||||

Db 61 CWDGLMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTGFRETVEYLV 120
   |||||||
QY 156 CWDGLMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTGFRETVEYLV 215

Db 121 SFGVWIRTPPAYPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
   |||||||
QY 216 SFGVWIRTPPAYPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 275

Db 181 SQC 183
   |||
QY 276 SQC 278

RESULT 9
ID 068068 PRELIMINARY; PRT; 212 AA.
AC 068068;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LICHERI-3'90;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85315; G736207; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24366 MW; AB227A9B CRC32;

Query Match
Best Local Similarity 98.9%; Score 1370; DB 14; Length 212;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAI 88
   |||||||
QY 95 SMDIDPKKFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAI 154
   |||||||

Db 89 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTGFRETVEYLV 148
   |||||||
QY 155 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTGFRETVEYLV 214
   |||||||

Db 149 VSRGWIRTPPAYPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
   |||||||
QY 215 VSRGWIRTPPAYPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 274

Db 209 ESQC 212
   |||
QY 275 ESQC 278

RESULT 10
ID 068025 PRELIMINARY; PRT; 212 AA.
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AC 068025;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTAG'3;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85293; G736126; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;

Query Match
Best Local Similarity 98.9%; Score 1370; DB 14; Length 212;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAI 88
   |||||||
QY 95 SMDIDPKKFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAI 154
   |||||||

Db 89 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTGFRETVEYLV 148
   |||||||
QY 155 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTGFRETVEYLV 214
   |||||||

Db 149 VSRGWIRTPPAYPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
   |||||||
QY 215 VSRGWIRTPPAYPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 274

Db 209 ESQC 212
   |||
QY 275 ESQC 278

RESULT 11
ID 067872 PRELIMINARY; PRT; 212 AA.
AC 067872;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE C/C ORF.
GN HEPATITIS B VIRUS.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT C, HBSAG POSITIV, HBV SUBTYPE ATW;
RA LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A., PORRU A.;
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65257; G59431; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24348 MW; A6BD9DA1 CRC32;

Query Match
Best Local Similarity 98.4%; Score 1369; DB 14; Length 212;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAI 88
   |||||||
QY 95 SMDIDPKKFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAI 154
   |||||||

Db 89 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTGFRETVEYLV 148
   |||||||
QY 155 LCGELMTLATWGVNLEDPASRDLYSVYNTNMGKFRQLMFHISCLTGFRETVEYLV 214
   |||||||

Db 149 VSRGWIRTPPAYPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
   |||||||
QY 215 VSRGWIRTPPAYPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 274

Db 209 ESQC 212
```

QY 275 ESOC 278
|||||
RESULT 12
ID 067984 PRELIMINARY; PRT: 212 AA.
AC 067984;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT VITORINA'92:
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85256; G736052; -.
PR PAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24322 MW; 83d9780b CRC32;
Query Match 65.6%; Score 1369; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 4.30e-225;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALROAI 88
QY :|||||
95 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALROAI 154
Db 89 LCMGELMTLATWGVNLEDASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 148
QY :|||||
155 LCMGELMTLATWGVNLEDASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 214
Db 149 VSEGVWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 208
QY :|||||
215 VSEGVWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 274
Db 209 ESOC 212
QY :|||||
275 ESOC 278
RESULT 13
ID 068032 PRELIMINARY; PRT: 212 AA.
AC 068032;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CHIGINE-2'86;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85296; G736139; -.
PR PAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24308 MW; 69d87b53 CRC32;
Query Match 65.6%; Score 1369; DB 14; Length 212;
Best Local Similarity 98.4%; Pred. No. 4.30e-225;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALROAI 88
QY :|||||
95 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALROAI 154
Db 89 LCMGELMTLATWGVNLEDASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 148
QY :|||||

QY 155 LCMGELMTLATWGVNLEDASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 214
Db 149 VSEGVWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 208
QY :|||||
215 VSEGVWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 274
Db 209 ESOC 212
QY :|||||
275 ESOC 278
RESULT 14
ID 068010 PRELIMINARY; PRT: 212 AA.
AC 068010;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT FERRACUTI-2'90;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85285; G736100; -.
PR PAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24292 MW; 04a4d12d CRC32;
Query Match 65.5%; Score 1368; DB 14; Length 212;
Best Local Similarity 98.4%; Pred. No. 6.64e-225;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALROAI 88
QY :|||||
95 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALROAI 154
Db 89 LCMGELMTLATWGVNLEDASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 148
QY :|||||
155 LCMGELMTLATWGVNLEDASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVEYL 214
Db 149 VSEGVWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 208
QY :|||||
215 VSEGVWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 274
Db 209 ESOC 212
QY :|||||
275 ESOC 278
RESULT 15
ID 068070 PRELIMINARY; PRT: 212 AA.
AC 068070;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT GIORDO'84;
RA LAI M.E., MAZOLENT A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85316; G736210; -.
PR PAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24376 MW; 80f52d0f CRC32;
Query Match 65.4%; Score 1366; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.58e-224;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

US3890-10-38183
MDIDPYKEFGATVEELLSFLPSDFPVSVDLDTASALYREALSPHHTALROAILCWEELMTLAT
WGVNLEDPASRDVVSYNLLQMDFGPEHLVDFLQSLMDIDPYKEFGATVEELLSFLPSDFPVS
DLDTASALYREALSPHHTALROAILCWEELMTLATWGVNLEDPASRDVVSYNLLQMDKFR
OLMFIHISCLTFEGRETVIEYVFCWMIIRTPPAYRPNAPILSTLPETTVARRGRSPRRRTPSRRRS
OSPRRRRSQSRSSQ1

 N O T E S

 (TW)

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 Msrch_DP protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 16 13:44:26 1999; MasPar time 13.43 Seconds

Tabular output not generated. 467.254 Million cell updates/sec

Title: >US3890-10-38183
 Description: (1-295) from us3890-10-38183.pep
 Perfect Score: 2205
 Sequence: 1 MDIDYKEGATVELLSFP.....RRRSQSPRRRSQSRHSQC 295

Scoring table: PAM 150
 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 33.363; Variance 173.459; scale 0.192

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1375	62.4	194	32	W50242	Hepatitis B virus pre
2	1375	62.4	212	32	W50250	Hepatitis B virus pre
3	1375	62.4	346	5	R27473	S12/core protein.
4	1363	61.8	184	1	P80959	Hepatitis B virus sub
5	1358	61.6	183	32	W50251	Hepatitis B virus p21
6	1359	61.6	193	32	W50241	Hepatitis B virus pre
7	1353	61.4	183	20	W09044	Hepatitis B virus cor
8	1349	61.2	183	1	R05635	Hepatitis B antigen.
9	1349	61.2	183	5	P00041	Sequence of core anti
10	1344	61.0	397	20	W09048	Plasmid pHBV DN Aa en
11	1338	60.7	184	5	P00004	Sequence of core anti
12	1336	60.6	196	8	R40806	Hepatitis B core / PV
13	1337	60.6	208	8	R40808	Hepatitis B core / PV
14	1334	60.5	183	4	P40311	Hepatitis B virus cor
15	1334	60.5	183	8	R40805	Hepatitis B core prot
16	1334	60.5	183	13	R68868	Hepatitis B virus pol

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
1	W50242	60.5	183	12	R62869	Hepatitis B virus cor	2.91e-96
2	W50242	60.5	198	8	R40807	Hepatitis B core / TL	3.32e-96
3	W50242	60.2	293	10	R5286	Presi full length cor	9.02e-96
4	W50242	60.1	183	13	R68866	Hepatitis B virus pol	1.59e-95
5	W50242	60.1	214	1	P90702	Deduced amino acid se	1.59e-95
6	W50242	60.1	289	20	W09049	Plasmid pHBV DN BB en	1.59e-95
7	W50242	60.0	185	6	R30861	Hepatitis B core anti	1.92e-95
8	W50242	60.0	185	10	R5284	Deduced sequence of f	1.92e-95
9	W50242	60.0	185	6	R30780	Native HBcAg protein.	1.92e-95
10	W50242	60.0	185	6	R31025	Native HBcAg protein.	1.92e-95
11	W50242	59.9	183	13	R68869	Hepatitis B virus pol	4.07e-95
12	W50242	59.9	185	26	P30061	Core antigen of HBV.	3.37e-95
13	W50242	59.7	185	6	R30781	Altered HBcAg protein	7.16e-95
14	W50242	59.7	185	6	R31026	Altered HBcAg protein	7.16e-95
15	W50242	59.6	183	13	R68867	Hepatitis B virus pol	1.26e-94
16	W50242	59.5	183	13	R68870	Hepatitis B virus pol	1.52e-94
17	W50242	59.5	185	6	R30784	Altered HBcAg protein	2.21e-94
18	W50242	59.5	185	6	R31029	Altered HBcAg protein	2.21e-94
19	W50242	59.5	185	6	R30865	Modified hepatitis B	2.21e-94
20	W50242	59.5	185	6	R30865	Modified hepatitis B	2.21e-94
21	W50242	59.4	185	6	R31028	Hepatitis B core anti	3.23e-94
22	W50242	59.3	185	6	R30783	Altered HBcAg protein	3.89e-94
23	W50242	59.3	185	6	R30864	Modified hepatitis B	3.89e-94
24	W50242	59.1	214	1	P80961	HBV core antigen enco	9.98e-94
25	W50242	59.0	203	1	P82872	HBcAg/beta-gal fusion	1.20e-93
26	W50242	58.4	198	32	W50252	Hepatitis B virus pre	2.03e-92
27	W50242	57.3	183	17	R68878	Hepatitis B virus E a	1.85e-90
28	W50242	57.1	183	17	R68883	Hepatitis B virus E a	3.99e-90
29	W50242	57.1	183	17	R68884	Hepatitis B virus E a	4.74e-90

RESULT 1
 ID W50242 standard; Protein; 194 AA.

AC W50242; 28-SEP-1998 (first entry)

DE Hepatitis B virus precore p22 polypeptide Met-p22.

KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;

KW hepatocyte; liver; Met-p22.

OS Hepatitis B virus.

OS Synthetic.

FT Key Location/Qualifiers

FT Protein 2..194

FT 12-MAR-1998. /Label- p22

PD W09809649-A1.

PF 03-SEP-1997; U15500.

PR 03-SEP-1996; US-025370.

PA (GEHO) GEN HOSPITAL CORP.

PI Melegari M, Scaglioni PP, Wands JR;

DR WPR: 98-19325/17.

PT DNA encoding proteins which can be incorporated with wild type

PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for

PT inhibition of viral replication, especially hepatitis B virus

PS Claim 11; Page 40; 60pp; English.

CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)

CC protein with an added N-terminal Met residue; p22 is produced by

CC elimination of the 19-amino acid leader peptide from the 25 kDa

CC full-length HBV precore protein (see W50250). Evidence is provided

CC that HBV replication is inhibited in the presence of high levels of

CC HBV precore or precore-related proteins. These proteins can be

CC incorporated into HBV nucleocapsids along with the p1 core protein

CC (see W50251), which is the usual nucleocapsid component, and

CC thereby render the nucleocapsids deficient in encapsidating HBV

CC pregenomic RNA. Thus, over-expression of the precore proteins, or

CC certain variants of them, leads to transdominant inhibition of HBV

CC replication. Suitable inhibitory proteins include p25 (see W50250),

CC p22, Met-p22, p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het

CC (see W50238). Heterologous peptides (see W50244-49) may be

CC inserted into the p22 and Met-p22 polypeptides. The inhibitory

CC proteins can be produced by recombinant methods using claimed

CC expression vectors and host cells. They can be provided exogenously

CC to the target cells for use in inhibiting HBV replication.
CC Alternatively, a nucleic acid construct that directs overexpression
CC of an inhibitory protein in target cells is used for the gene
CC therapy of HBV infection.
SQ Sequence 194 AA:

Query Match 62.4%; Score 1375; DB 32; Length 194;

Best Local Similarity 99.5%; Pred. No. 1.29e-99;

Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 gmdidykefgatvelsfpsdfsvrdldgtasalyrealsepshcphntalrgai 70

OY 112 SMIDPKKEGATVELLSFSPDFSVRDLDTASALYREALSEPCHCSPHNTALROAI 171

OY 172 LCWGEIMLTATWGVNLDEPARDLVSVYNTMGLKFRQLMFHISCLTFGRETYEYL 231

Db 131 vsfgwvrtppayrpnpnaillstlpettvrrrgsrprtrpsrrrrsgsr 190

OY 232 VSGGWIRTPAPRPAPNPAILSTLPETTIVRRRGSRPRRTSPRRRSQSPRRRSQSR 291

Db 191 esgc 194

OY 292 ESQC 295

RESULT 2

ID W50250 standard; Protein: 212 AA.

AC W50250:

DT 28-SEP-1998 (first entry)

DE Hepatitis B virus precore p25 polypeptide.

KW Hepatitis B virus replication; inhibitor; HBV; nucleocapsid; gene therapy;

KW hepatocyte; liver; p25 protein.

OS Hepatitis B virus.

PN MO9809649-A1.

PD 12-MAR-1998.

PE 03-SEP-1997; 015500.

PR 03-SEP-1996; US-025370.

PA (GHEO) GEN HOSPITAL CORP.

PI Melegari M, Scaglioni P, Wands JR;

DR WPI: 98-193325/17

PT DNA encoding proteins which can be incorporated with wild type

PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for

PT inhibition of viral replication, especially hepatitis B virus

PS Claim 15: Page 35; 60pp; English.

CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)

CC protein that is encoded by the full-length HBV precore gene.

CC Evidence is provided that HBV replication is inhibited in the

CC presence of high levels of HBV precore or precore-related proteins.

CC These proteins can be incorporated into HBV nucleocapsids along

CC with the p21 core protein (see W50251), which is the usual

CC nucleocapsid component, and thereby render the nucleocapsids

CC deficient in encapsidating HBV pregenomic RNA. Thus, over-

CC expression of the precore proteins, or certain variants of them,

CC leads to transdominant inhibition of HBV replication. Suitable

CC inhibitory proteins include p25, p22 (see W50241), Met-p22 (see

CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het

CC (see W50238). The inhibitory proteins can be produced by

CC recombinant methods using claimed expression vectors and host

CC cells. They can be provided exogenously to the target cells for

CC use in inhibiting HBV replication. Alternatively, a nucleic acid

CC construct that directs overexpression of an inhibitory protein in

CC target cells is used for the gene therapy of HBV infection.

SQ Sequence 212 AA:

Query Match 62.4%; Score 1375; DB 32; Length 212;

Best Local Similarity 99.5%; Pred. No. 1.29e-99;

Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 gmdidykefgatvelsfpsdfsvrdldgtasalyrealsepshcphntalrgai 88

OY 112 SMIDPKKEGATVELLSFSPDFSVRDLDTASALYREALSEPCHCSPHNTALROAI 171

Db 89 lwcwgeimltatwgvnldepardlvsvyntmglkfrqlmfhisccltfgretyeyl 148

OY 172 LCWGEIMLTATWGVNLDEPARDLVSVYNTMGLKFRQLMFHISCLTFGRETYEYL 231

Db 149 vsfgwvrtppayrpnpnaillstlpettvrrrgsrprtrpsrrrrsgsr 208

OY 232 VSGGWIRTPAPRPAPNPAILSTLPETTIVRRRGSRPRRTSPRRRSQSPRRRSQSR 291

Db 209 esgc 212

OY 292 ESQC 295

RESULT 3

ID R27473 standard; Protein: 346 AA.

AC R27473:

DT 24-FEB-1993 (first entry)

DE S12/core protein.

KW Hepatitis B virus; HBV; M protein; small pre-S antigen; spsag;

KW Vaccinia virus; I3L; promoter; NVVAC; recombinant; HBV L;

KW large pre-S antigen; Ipsag; fusion protein; pre-S region; S12/core;

KW S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;

KW deletion loci; recipient loci.

OS Synthetic.

FH Key Location/Qualifiers

FT region 1..108

FT region 109..163

FT region 164..346

FT region /label= S2

FT region /label= Core

PN WO9215672-A.

PD 17-SEP-1992.

PE 09-MAR-1992; U01906.

PR 07-MAR-1991; US-666056.

PR 11-JUN-1991; US-713967.

PR 06-MAR-1992; US-847951.

PA (VIRO-) VIROGENETICS CORP.

PI Cox MI, De Taisne C, Francis J, Gettig RR, Johnson GP,

PI Limbach KJ, Norton EK, Paolletti E, Perkins ME, Plancus SE,

PI Riviere M, Tartaglia J, Taylor J;

DR WPI: 92-331718/40.

PT N-PSDB: Q29105.

PT Vaccine comprises recombinant, attenuated pox-virus - use for

PT vaccinating against viral infections such as rabies, hepatitis B,

PT HIV, HSV, EBV, CMV, mumps etc.

PS Disclosure: Fig 13; 45pp; English.

CC The sequence given is encoded by an expression cassette which

CC comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/

CC core) which is precisely linked to the I3L promoter derived from

CC vaccinia virus. This DNA sequence was linked to the S1 and S2

CC sequences and this fragment was used in the construction of a NVVAC

CC recombinant expressing the HBV gene. Other HBV genes were also used

CC in the construction. These were HBV M protein (small pre-S antigen,

CC spsag) and HBV L (large pre-S antigen, Ipsag). Each of these gene

CC sequences were inserted individually into three different sites of

CC NVVAC separated by from each other by large regions of vaccinia DNA

CC containing essential genes. NVVAC is a Copenhagen vaccine strain of

CC vaccinia virus which has been modified by deletion of six non-essential

CC regions of the genome encoding known or potential virulence factors.

CC The deletion loci were engineered as recipient loci for the insertion

CC of foreign genes. The spacing of the three inserted sequences ensured

CC that any recombination that did occur would lead to disruption of the

CC vaccinia genome and would cause unviable vaccinia virus. See also

SQ Sequence 346 AA:

Query Match 62.4%; Score 1375; DB 5; Length 346;

Best Local Similarity 99.5%; Pred. No. 1.29e-99;

Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 163 mndidykefgatvelsfpsdfsvrdldgtasalyrealsepshcphntalrgai 222

Query March	61.8%	Score 1363	DB 1	Length 184
Best Local Similarity	99.5%	Pred. No. 1,24e-96		
Matches 153	Conservative	0	Mismatches 0	Indels 1
				Gaps 1
Db	1	mdlpykefgatveljstfpedffpsvrdldtsaalyrealespehcsphitelrgail	60	
QY	113	MDIPYKEFGATVELSTLSPDSDFPSVVDLDTASALYREALSEPEHCSPHHTLRQAIL	172	
Db	61	cmwglmtlatvngvnledpasrdlvsvyotnmajkfqqlwlwfhscitlffgretvleyl	120	
QY	173	CMWGLMTLATVNGVNLDPASRDLVSVYNTNMJLKRQLLMWFHISCLTF-GRETVLEYL	231	
Db	121	vsfgwiltprayrppnapilstlipeetvtrirgsprrtpprrrrsgspprrrrsgsr	180	
QY	232	VSFGWILTPRAYRPPNAPILSTLIPETTVVARRGRSPRRRIPSPRRRRSQSPRRRRQSR	291	
Db	181	esqc 184		
QY	292	ESQC 295		

Query Match	61.6%	Score 1358;	DB 32;	Length 183;
Best Local Similarity	98.9%	Pred. No. 3,17e-98;		
Matches 181;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Db 1	mdidykxfgatvaelisflpsdfpsvrdltdcasalyrealaspehscphthalrqa1	60		
Qy 113	MDIDPYKFGATVELLSFLPSDFPSVRDLDTASALYREALESPCHSPHTALRQAIL	172		
Db 61	cwgelmtlactwgyvnlcdpasrdlwsyvdtimglkrtqllwfmisc1tqretvleylv	120		
Qy 173	CWGE1MTLACTWGVNLCDPASRD1WSYVDTIMG1KRTQ1LWFMISC1TQRETVE1YLV	232		
Db 121	sfgwrtktpvprppnapi1st1pctvtvrrrrgrspprrtsprrrrgspprrrrgsre	180		
Qy 233	SFGWRTKTPVPRPRPNAPI1ST1PCTVTVRRRRGRSPRRRTPSPRRRRGSRR	292		
Db 181	sqc 183			
Qy 293	SQC 295			

PF 03-SEP-1997; U15500.
 PR 03-SEP-1996; US-025370.
 PA (GHEO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR:
 DR WPI; 98-193325/17.
 PT DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus
 PS Claim 9: Page 34-35: 60pp: English.
 CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
 CC protein that is produced by elimination of the 19-amino acid leader
 CC peptide from the 25 kDa full-length HBV precore protein (see
 CC W50250). Evidence is provided that HBV replication is inhibited in
 CC the presence of high levels of HBV precore or precore-related
 CC proteins. These proteins can be incorporated into HBV nucleocapsids
 CC along with the p21 core protein (see W50251), which is the usual
 CC nucleocapsid component, and thereby render the nucleocapsids
 CC deficient in encapsidating HBV pregenomic RNA. Thus, over-
 CC expression of the precore proteins, or certain variants of them,
 CC leads to transdominant inhibition of HBV replication. Suitable
 CC inhibitory proteins include p25 (see W50250), p22, Met-p22 (see
 CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
 CC (see W50238). Heterologous peptides (see W50244-49) may be
 CC inserted into the p22 and Met-p22 polypeptides. The inhibitory
 CC proteins can be produced by recombinant methods using claimed
 CC expression vectors and host cells. They can be provided exogenously
 CC to the target cells for use in inhibiting HBV replication.
 CC Alternatively, a nucleic acid construct that directs overexpression
 CC of an inhibitory protein in target cells is used for the gene
 CC therapy of HBV infection.
 SQ Sequence 193 AA;

Query Match 61.6%; Score 1359; DB 32; Length 193;
 Best Local Similarity 98.4%; Pred. No. 2.63e-98;
 Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 10 gmdipkyefgatvellsfipsdffsvrdllltasalyrealespeshcphtalrqal 69
 :|||||
 QY 112 SMDIPKKEGATVELLSFIPSDFFSVRDLLDTASALYREALESPHCSPHHTALRQAI 171
 Db 70 lcgwelmrlatwgvnledpasrdlvsvyrdtmqkfrqlwfhscldfgetvleyl 129
 :|||||
 QY 172 LCGWELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLWFMHISCLFGETVLEYL 231
 Db 130 vsfgvwlrtppayrppnapilslpettvtvrrgrrpsrrrrsgsrrrrsgsr 189
 :|||||
 QY 232 VSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSR 291
 Db 190 esgc 193
 :|||
 QY 292 ESQC 295

RESULT 7
 ID W09044 standard; Protein: 183 AA.
 AC W09044;
 DT 11-APR-1997 (first entry)
 DE Hepatitis B virus core protein.
 DE Hepadnavirus; HBV; woodchuck hepatitis virus; hepatitis delta virus;
 KW ground squirrel hepatitis B virus; duck hepatitis B virus;
 KW core protein; replication; antiviral; gene therapy.
 OS Hepatitis B virus.
 FH Hepatitis B virus.
 FT misc-difference 71..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 71-180 in mutant
 FT polypeptides of the invention (Claim 23)"
 FT 81..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 81 and 180 in mutant
 FT polypeptides of the invention (Claim 5)"
 FT 171..180
 FT /note= "C-terminus of core protein is at any amino

FT acid position between 171 and 180 in mutant
 FT polypeptides of the invention (Claim 6)"
 FT 174..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 174 and 180 in mutant
 FT polypeptides of the invention (Claim 26)"
 FT 178
 FT /note= "C-terminus of core protein is at amino acid
 FT position 178 in mutant polypeptides of the
 FT invention (Claim 7)"
 FT 178
 FT /note= "C-terminus of core protein is at amino acid
 FT position 178 in mutant polypeptides of the
 FT invention (Claim 7)"
 FT 178
 FT /note= "C-terminus of core protein is at amino acid
 FT position 178 in mutant polypeptides of the
 FT invention (Claim 7)"
 FT 172..183
 FT /note= "amino acid residues 172-183, pref. 174-180,
 FT are deleted from the core protein in mutant
 FT polypeptides of the invention"

PN W09700698-A1.
 PD 09-JAN-1997.
 PF 20-JUN-1996; U10602.
 PR 20-JUN-1995; US-017814.
 PA (GHEO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR:
 DR WPI; 97-087176/08.
 DR N-PSDB; T49594.

PT New method for inhibiting the replication of hepadnaviruses -
 PT comprises introducing a mutant polypeptide with a mutated core
 PT protein or corresponding nucleic acid, for treating, e.g. hepatitis
 PS B
 PS Claim 5: Page 55-56; 83pp: English.
 CC Alteration of the C-terminus of the core protein (W09044) of
 CC hepatitis B virus (HBV) or other hepadnavirus creates a mutant
 CC polypeptide capable of reducing replication of the wild-type virus
 CC by a dominant negative mechanism. The inhibitory effect is
 CC species-specific and is achieved by deletion of a few C-terminal
 CC amino acids from the core protein, and/or by joining the core
 CC protein to a hepadnavirus surface protein (see also W09045),
 CC creating a core-surface fusion. Such mutant polypeptides (see
 CC also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
 CC infection.
 SQ Sequence 183 AA;

Query Match 61.4%; Score 1353; DB 20; Length 183;
 Best Local Similarity 98.9%; Pred. No. 8.14e-98;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 mididpykefgatvellsfipsdffsvrdllltasalyrealespeshcphtalrqal 60
 :|||||
 QY 113 MDIDPYKEFGATVELLSFIPSDFFSVRDLLDTASALYREALESPHCSPHHTALRQAIL 172
 Db 61 cwgelmrlatwgvnledpasrdlvsvyrdtmqkfrqlwfhscldfgetvleyl 120
 :|||||
 QY 173 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLWFMHISCLFGETVLEYL 232
 Db 121 sfvgvwlrtppayrppnapilslpettvtvrrgrrpsrrrrsgsrrrrsgsre 180
 :|||||
 QY 233 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSR 292
 Db 181 sqc 183
 :|||
 QY 293 SQC 295

RESULT 8
 ID R05635 standard; protein: 183 AA.
 AC R05635;
 DT 30-OCT-1990 (first entry)
 DE Hepatitis B antigen.
 DE Hepatitis B virus; vaccine; HBV; ds.
 KW Hepatitis B virus; vaccine; HBV; ds.
 OS Synthetic.
 PN EP-374869-A.
 PD 27-JUN-1990.

PF 1-JAN-1989; 123526.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOJ) Biogen Inc.
PI Murray K, Schaller HE;
DR WPI: 90-195067/26.
N-PSDB: 004799.
PT Recombinant DNA encoding Hepatitis B virus polypeptide antigens -
PS used in detection of infection and in vaccine prodn.
PT Disclosure: 4pp; English.
CC Polypeptide fragments encoded by the DNA sequence are antigenic for
CC HBV and may be used as a vaccine or in detection. Peptides may be
CC cultured in a suitable bacterial host such as E.coli.
CC Fragments of the sequence are also claimed as being antigenically
CC useful.
SQ Sequence 183 AA:

Query Match 61.2%; Score 1349; DB 1; Length 183;
Best Local Similarity 96.7%; Pred. No. 1.73e-97;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdipykefgatvellsfipdsffpsvrdldtaaalrydalespeshphthalrgail 60
|||
QY 113 MDIDPYKEFGATVELLSFIPDSFFPSVARDLDTASALYREALSEPHCSPHHTALRQAIL 172
|||
Db 61 cwgdlmtlatwgvnlgedpasrdlvsvyvnmgkfrqlwfhlscltfgretvleylv 120
|||
QY 173 CWGELMTLATWGVNLGEDPASRDLVSVYVNTMGLKFRQLWFMHISCLTFGRETVIEYLV 232
|||
Db 121 sfgywlrtppayrpnpaillstlpetvrrrgsrprrrrrpsrrrrsgsr 180
|||
QY 233 SFGWIRTPPAYRPPNAILSTLPETTVRRRGSRPRRRTPSPRRRSQSPRRRSQSRE 292
|||
Db 181 sqc 183
|||
QY 293 SQC 295

RESULT 9
ID P00041 standard; Protein; 183 AA.

AC P00041; 1992 (first entry)
DT 14-OCT-1992
DE Sequence of core antigen.
KW Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
OS Hepatitis B virus.
PN EP-13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979; 303017.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOJ) Biogen Inc.
PI Murray K, Schaller HE;
DR WPI: 80-57268C/33.
N-PSDB: N00003.
PT Recombinant DNA coding for polypeptide - have specificity of
PT hepatitis B viral antigens in detection or antibody stimulation
PS Example; Figs 3-4; 43pp; English.
CC Human serum from a single HBsAg positive, HBeAg positive donor
CC (serotype adym) was used to prep. a DNA-contg. pellet which was
CC labelled with 3H or 32P as described by P. M. Kaplan et al (1973).
CC The labelled DNA was then extracted with phenol from the resulting
CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
CC It was then cloned in plasmid pBR322 which was used to transform E.
CC coli. Micro-organisms prepd. by the processes are deposited at the
CC NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dg:
CC HBV-Kpn I dg: Tetr Amps HBV+.
SQ Sequence 183 AA:

Query Match 61.2%; Score 1349; DB 5; Length 183;
Best Local Similarity 96.7%; Pred. No. 1.73e-97;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdipykefgatvellsfipdsffpsvrdldtaaalrydalespeshphthalrgail 60
|||
QY 113 MDIDPYKEFGATVELLSFIPDSFFPSVARDLDTASALYREALSEPHCSPHHTALRQAIL 172
|||
Db 61 cwgdlmtlatwgvnlgedpasrdlvsvyvnmgkfrqlwfhlscltfgretvleylv 120
|||
QY 173 CWGELMTLATWGVNLGEDPASRDLVSVYVNTMGLKFRQLWFMHISCLTFGRETVIEYLV 232
|||
Db 121 sfgywlrtppayrpnpaillstlpetvrrrgsrprrrrrpsrrrrsgsr 180
|||
QY 233 SFGWIRTPPAYRPPNAILSTLPETTVRRRGSRPRRRTPSPRRRSQSPRRRSQSRE 292
|||
Db 181 sqc 183
|||
QY 293 SQC 295

RESULT 10
ID W09048 standard; Protein; 397 AA.

AC W09048;
DT 11-APR-1997 (first entry)
DE Plasmid pHBV DN AA encoded HBV dominant negative polypeptide.
KW Hepadnavirus; woodchuck hepatitis virus; hepatitis delta virus;
KW HBV; ground squirrel hepatitis B virus; duck hepatitis B virus;
KW core protein; replication; antiviral; gene therapy; pHBV DN AA.
OS Hepatitis B virus.
FH Key
FT Location/Qualifiers
FT 1..179
FT /label= HBV_core
FT /note= "positions 1-179 correspond to amino acids
FT 1-179 of HBV core protein"
FT 180..397
FT /note= "positions 180-397 correspond to amino
FT acids 9-226 of HBV surface protein"

PN W09700698-A1.
PD 09-JAN-1997.
PF 20-JUN-1996; U10602.
PR 20-JUN-1995; US-017814.
PA (GENO) GEN HOSPITAL CORP.
PI Melegari M, Scaglioni PP, Wands JR;
DR WPI: 97-087176/08.
N-PSDB: T49598.
PT New method for inhibiting the replication of hepadnaviruses -
PT comprises introducing a mutant polypeptide with a mutated core
PT protein or corresponding nucleic acid, for treating, e.g. hepatitis
PT B.
PS Disclosure: Page 46-48; 83pp; English.
CC Plasmid pHBV DN AA carries an insert (T49598) coding for a protein
CC (W09048) comprising a hepatitis B virus (HBV) core protein (see
CC also W09044) fused in-frame at amino acid 179 with the HBV surface
CC protein (see also W09045) at amino acid 8. Plasmid pHBV DN BB
CC (T49599) expresses the HBV core fused at amino acid 175 to the
CC surface protein at amino acid 112 (W09049). pHBV DN AA was at
CC least as potent an inhibitor of HBV replication as construct
CC pHBV DN (T49597); pHBV DN BB was less inhibitory than pHBV DN.
CC Vectors expressing hepadnavirus dominant negative core mutants can
CC be utilised in the gene therapy of viral infections.
SQ Sequence 397 AA:

Query Match 61.0%; Score 1344; DB 20; Length 397;
Best Local Similarity 100.0%; Pred. No. 4.43e-97;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mdipykefgatvellsfipdsffpsvrdldtaaalrydalespeshphthalrgail 60
|||
QY 113 MDIDPYKEFGATVELLSFIPDSFFPSVARDLDTASALYREALSEPHCSPHHTALRQAIL 172
|||
Db 61 cwgdlmtlatwgvnlgedpasrdlvsvyvnmgkfrqlwfhlscltfgretvleylv 120
|||
QY 173 CWGELMTLATWGVNLGEDPASRDLVSVYVNTMGLKFRQLWFMHISCLTFGRETVIEYLV 232
|||
Db 121 sfgywlrtppayrpnpaillstlpetvrrrgsrprrrrrpsrrrrsgsr 179
|||

QY 233 SFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291

RESULT 11
ID P00004 standard: Protein; 184 AA.

AC P00004; 14-OCT-1992 (first entry)
DE Sequence of core antigen.
KM Hepatitis B virus: antigen; antibody; diagnosis; vaccine.
OS Hepatitis B virus.

PN EP-13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979; 303017.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOI) BIOGEN NV.
PI Murray K. Schaller HE;
DR WPI: 80-57268C/33.
N-PSDB: N00002.

PT Recombinant DNA coding for polypeptide - have specificity of hepatitis B viral antigens in detection or antibody stimulation
PS Claim 13: Page 40; 43pp; English.
CC Human serum from a single HBsAg positive, HBeAg positive donor (serotype adym) was used to prep. a DNA-contg. pellet which was labelled with 3H or 32P as described by P. M. Kaplan et al (1973).
CC The labelled DNA was then extracted with phenol from the resulting pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
CC It was then cloned in plasmid pBR322 which was used to transform E. coli. Micro-organisms prepd. by the processes are deposited at the CC NCB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dg:
CC HBV-Kpn I dc: Tetr Amps HBV+.
SQ Sequence 184 AA;

Query Match 60.7%; Score 1338; DB 5; Length 184;
Best Local Similarity 96.2%; Pred. No. 1.37e-96;

Matches 177; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

DB 1 mdidpykefgasvellsfipdsffpsvrcdlldtaaalysalesephecsphthalrqa 60
QY 113 MDIDPYKEFGATVELLSLPSDFPSV-RDLDPRASALYREALSEPHCSPHHTALRQA 171
DB 61 lwcgdlmlatwgnledpasrdlvsyvntnglkirqlwfhisccltfgretvleyl 120
QY 172 LWCGLMLATWGNLEDPASRDLVSVYNTNGLKFROLWFHISCCLTFGRETVEYL 231
DB 121 vsfgvwtppayrppnapilstlpettvrrrrgsprrrrrrrrrrrrrrrrrrrrrrr 180
QY 232 VSFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291
DB 181 esgc 184
QY 292 ESQC 295

RESULT 12

ID R40806 standard: Protein; 196 AA.

AC R40806; 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 fusion.
KM Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Synthetic.

FH Key Location/Qualifiers
FT region 7..13
FT protein /label= PV-1
FT /label= HBC

PN J05192170-A.
PD 03-AUG-1993.
PF 24-SEP-1991; 243800.
PR 24-SEP-1991; JP-243800.
PA (NISM) NISSHIN OIL MILLS LTD.

DR WPI: 93-277479/35.

DR N-PSDB: Q47736.

PT Recombinant plasmid for high immunogenicity virus - contains recombinant haemagglutinin gene, hepatitis B core gene of vaccinia virus and exotic genes

PS Disclosure; Fig 7; 12pp; Japanese.

CC The hepatitis B core gene is recombinant with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce a vaccine. NB: Sequence is difficult to read in the original
CC Specification.
SQ Sequence 196 AA;

Query Match 60.6%; Score 1336; DB 8; Length 196;
Best Local Similarity 95.1%; Pred. No. 2.00e-96;

Matches 175; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

DB 13 amdidpykefgasvellsfipdsffpsvrcdlldtaaalysalesephecsphthalrqa 72
QY 112 SMDIDPYKEFGATVELLSLPSDFPSV-RDLDPRASALYREALSEPHCSPHHTALRQA 171
DB 73 lwcgdlmlatwgnledpasrdlvsyvntnglkirqlwfhisccltfgretvleyl 132
QY 172 LWCGLMLATWGNLEDPASRDLVSVYNTNGLKFROLWFHISCCLTFGRETVEYL 231
DB 133 vsfgvwtppayrppnapilstlpettvrrrrgsprrrrrrrrrrrrrrrrrrrrrrr 192
QY 232 VSFGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291
DB 193 esgc 196
QY 292 ESQC 295

RESULT 13
ID R40808 standard: Protein; 208 AA.

AC R40808; 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 / IL-1 Fusion.
KM Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Synthetic.

FH Key Location/Qualifiers
FT region 8..19
FT /label= PV-1
FT /label= IL-1
FT protein /label= HBC

PN J05192170-A.
PD 03-AUG-1993.
PF 24-SEP-1991; 243800.
PR 24-SEP-1991; JP-243800.
PA (NISM) NISSHIN OIL MILLS LTD.
DR WPI: 93-277479/35.
DR N-PSDB: Q47738.
PT Recombinant plasmid for high immunogenicity virus - contains recombinant haemagglutinin gene, hepatitis B core gene of vaccinia virus and exotic genes
PS Disclosure; Fig 9; 12pp; Japanese.
CC The hepatitis B core gene is recombinant with PV-1 DNA
CC and IL-1 beta to form a plasmid (Q47738) which is then used to produce a vaccine. NB: Sequence is difficult to read in the original
CC Specification.
SQ Sequence 208 AA;

Query Match 60.6%; Score 1337; DB 8; Length 208;
Best Local Similarity 94.6%; Pred. No. 1.66e-96;

Matches 175; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

DB 24 lmdidpykefgasvellsfipdsffpsvrcdlldtaaalysalesephecsphthalrqa 83
QY 111 LMDIDPYKEFGATVELLSLPSDFPSV-RDLDPRASALYREALSEPHCSPHHTALRQA 170
DB 84 lwcgdlmlatwgnledpasrdlvsyvntnglkirqlwfhisccltfgretvleyl 143

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OY	171	ILCNGELMTLATWGVNLEDPASNDLVVSYNTNMGLKFRQLMFHISCLTFGEITYEX	230
Db	144	lvfsgvwtirpepayrppnaipilsclpettvtvrrgrsprrrtcpsprrrrsqsprrrrsqs	2038
OY	231	lvfsgvwtirpepayrppnapilsltpettvvrrrgsrpsrrrtbpsprrrrsosprrrrsos	2900
Db	204	rresgc 208	
OY	291	RESOC 295	

RESULT 14
ID PA0311 standard; Protein; 183 AA.
AC PA0311; 18-AUG-1992 (first entry)
DT 18-AUG-1992 (first entry)
DE Hepatitis virus core antigen.
OS HBcAg; vaccine; diagnosis; HBV infection.
KS Hepatitis b virus.
PN J59074985-A.
PD 27-APR-1984.
PE 19-OCT-1982; 183432.
PR 19-OCT-1982; JP-183432.
PA (TAKE) TAKEDA CHEMICAL IND KK.
DR WPI: 84-143231/23.
PT DNA used in prevention of infections by hepatitis virus B -
PT comprises structural gene of hepatitis virus adr B surface antigen
PT coding gene and at least 1 virus core antigen structural gene.
PS Disclosure: Fig 3; 13pp; Japanese.
CC The sequence is that of hepatitis virus core antigen (HBcAg) . It
CC can be used as a vaccine for the prevention of infections by
CC hepatitis B virus (HBV) and also in the diagnosis of early stages
CC of HBV infection. See also PA0310.
CC Sequence 183 AA;

Query Match	60.58;	Score 1334;	DB 4;	Length 183;
Best Local Similarity	95.60;	Pred. NO. 2.91e-96;		
Matches	175;	Conservative	5;	Mismatches 3; Indels 0; Gaps 0;

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Db      1 mdidpyvefgasvvalifijpedffpsrtdldtsaalayrealeespepcshatiraal 60
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy      113 MDIDPYVEFGATVLLSTFSPSDFPSPRDLDTASALYREALESPENCSPHNTLRQAAL 172
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 cweglmjlatwvsgnledpasrelvsvyvvnmnglkirtqlwfhtscitfgretvleylv 120
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy      173 CWGLMRLTATWGVNLDPASRDLVSVYVNTNMGLKRTQLMFWHTSCITFGRETVLEYLV 222
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      121 sfgywvlttppayrpnapilstlpetvrrirgrsprrrtppsprrrrsgsprrrrsgre 180
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy      233 SFGWVMTRPAYRPNPAPILSTLPEITVVRGRGSPRRPTSPRRRRSOSPRRRRSORE 292
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      181 sqc 183
      |||
Qy      293 SQC 295

```

RESULT	15
ID	R40805 standard; Protein; 183 AA.
AC	R40805;
DT	16-FEB-1994 (first entry)
DE	Hepatitis B core protein.
KW	Hepatitis B; core; HBC; PV-1; IL-1 beta; Interleukin; plasmid.
OS	Hepatitis B Virus.
PN	J05192170-A.
PD	03-AUG-1993.
PE	24-SEP-1991; 243800.
PR	24-SEP-1991; JP-243800.
PA	(NISW) NISSHIN OIL MILLS LTD.
DR	WPI: 93-277479/35.
NR	N-PDSB: 047735.
PT	Recombinant plasmid for high immunogenicity virus - contains
FT	recombined haemagglutinin gene, hepatitis B core gene of vaccinia
VT	virus and exotic genes

PS Disclosure: Fig 6: 12pp; Japanese.
CC The hepatitis B core gene is recombined with pV-1 DNA
CC and IL-1 beta to form a plasmid (p47738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.
SQ Sequence 183 AA:

Query Match	60.5%;	Score 1334;	DB 8;	Length 183;
Best Local Similarity	95.6%;	Pred. No. 2.91e-96;		
Matches 175;	Conservative 5;	Mismatches 3;	Indels 0;	Gaps 0;

Db	1	mdidpyvegsavallifpsdfpsrtdldtesaalgalsepncspbhcalraai	60
Qy	113	MDIDPYVEGSAVALLIFPSDFPSRDLDRASALREALSEPNCSPBHTRALRAIL	172
Db	61	cwgelmlnatwsgnledpasrelvsvyvnvmnglxlrqdlwfhiscitfgretvleylv	120
Qy	173	CWGEMLNATWVGNLBDDPASRLVSVYVNTMNGLKFRLMLFHISCLTFGRETVLEYLV	232
Db	121	sfgwvlttppayrppnaplisltpeltvrvrrrgsprrrtpprrrrsgpprrrrsgre	180
Qy	233	SFGWVIRTPPAYRPPNAPLISLTPELTIVRVRRGRSPRRRTPPRRRRSSQSPRRRRSSQRE	292
Db	181	sqc 183	
Qy	293	sqc 295	

Search completed: Thu Dec 16 13:47:38 1999
Job time : 192 secs.

##experimental_source isolate patient Licheri-1'85
#accession S53249
##molecule_type DNA
##residues 1-212 ##label LA5
##cross-references EMBL:X85306; NID:q736172; PID:q736174
##experimental_source isolate patient Fiore-1'86
#accession S53262
##molecule_type DNA
##residues 1-212 ##label LA6
##cross-references EMBL:X85312; NID:q736191; PID:q736193
##experimental_source isolate patient Licheri'83
#accession S53277
##molecule_type DNA
##residues 30-212 ##label LA7
##cross-references EMBL:X85317; NID:q736211; PID:q736214
##experimental_source patient Giordo-2'86
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be processed

REFERENCE
#authors Ag3214
Galibert, F.; Mandart, E.; Floussy, F.; Tiollais, P.;
Charnay, P.
#journal Nature (1979) 281:646-650
#title Nucleotide sequence of the hepatitis B virus genome (subtype
ayw) in E. coli.
#cross-references MUID:81012091
#accession A03711
##molecule_type DNA
##residues 1-212 ##label GAL
##cross-references GB:J02203; NID:q329640; PID:q329642
##experimental_source subtype ayw

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY
#length 212 #molecular-weight 24350 #checksum 782

Query Match 62.4%; Score 1375; DB 1; Length 212;
Best Local Similarity 99.5%; Pred. No. 8.67e-201;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLPASALYREALSPHCSPHHTALRQAI 88
QY 112 SMDIDPKKEGATVELLSFLPSDFPSVRLDLPASALYREALSPHCSPHHTALRQAI 171
Db 89 LCMGELMTLATWGVNEDPASRDVSVYNTNGLKFRQLMFHISCLTFGRETVEIYL 148
QY 172 LCMGELMTLATWGVNEDPASRDVSVYNTNGLKFRQLMFHISCLTFGRETVEIYL 231
Db 149 VSEGVWIRTPPAYRPPNAPILSTPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSR 208
QY 232 VSEGVWIRTPPAYRPPNAPILSTPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSR 291
Db 209 ESOC 212
QY 292 ESOC 295

RESULT 2
ENTRY S53207 #type complete
TITLE core antigen - hepatitis B virus (isolate patient
Castaa-2'87)
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Castaa-2'87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997 .

ACCESSIONS S53207
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53207
##molecule_type DNA
##residues 1-183 ##label LA1
##cross-references EMBL:X85289; NID:q736110; PID:q736113
##experimental_source isolate patient Castaa-2'87
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
SUMMARY #length 183 #molecular-weight 21102 #checksum 2165

Query Match 62.3%; Score 1373; DB 2; Length 183;
Best Local Similarity 99.5%; Pred. No. 1.88e-200;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKEGATVELLSFLPSDFPSVRLDLPASALYREALSPHCSPHHTALRQAI 60
QY 113 MDIDPKKEGATVELLSFLPSDFPSVRLDLPASALYREALSPHCSPHHTALRQAI 172
Db 61 CMGELMTLATWGVNEDPASRDVSVYNTNGLKFRQLMFHISCLTFGRETVEIYL 120
QY 173 CMGELMTLATWGVNEDPASRDVSVYNTNGLKFRQLMFHISCLTFGRETVEIYL 232
Db 121 SFGVWIRTPPAYRPPNAPILSTPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSRE 180
QY 233 SFGVWIRTPPAYRPPNAPILSTPETTVARRGRSPRRRTSPRRRSOSPRRRRSOSRE 292
Db 181 SOC 183
QY 293 SOC 295

RESULT 3
ENTRY S53211 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Castag-1'85 and others)
ALTERNATE_NAMES HBC antigen; HBe antigen precursor / HBe antigen; pre-C/C
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Castag-1'85; isolate patient Ferracuti-1'89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53211; S53197
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53211
##molecule_type DNA
##residues 1-212 ##label LA1
##cross-references EMBL:X85291; NID:q736117; PID:q736119
##experimental_source isolate patient Castag-1'85
#accession S53197
##molecule_type DNA
##residues 30-212 ##label LAW
##cross-references EMBL:X85284; NID:q736095; PID:q736098
##experimental_source isolate patient Ferracuti-1'89
#note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
30-178

179-212 #domain carboxyl-terminal propeptide #link EAG #status
 predicted #label ECP
SUMMARY #length 212 #molecular-weight 24336 #checksum 746

Query Match 62.3%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.28e-200;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPYKEFGATVELLSFLPSDFPSVVDLDTASALYREALSPHCSPHHTALRQAI 88
 |||||
OY 112 SMDIDPYKEFGATVELLSFLPSDFPSVVDLDTASALYREALSPHCSPHHTALRQAI 171
 |||||

DB 89 LCMGELMTLATVGVNLEDPASRDLYSVYNTNMGKLFKROLMLFHSCLTGFRETIVIEL 148
 |||||

OY 172 LCMGELMTLATVGVNLEDPASRDLYSVYNTNMGKLFKROLMLFHSCLTGFRETIVIEL 231
 |||||

DB 149 VSGFWIRTPPYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
 |||||

OY 232 VSGFWIRTPPYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 291
 |||||

DB 209 ESQC 212
 |||||

OY 292 ESQC 295

RESULT 4
ENTRY #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
 (subtype ayw, patient C1000)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
 #subtype ayw, patient C1000
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
 08-Sep-1997

ACCESSIONS
REFERENCE S32204
 S32202

GENETICS #gene
 #residues 1-212 #label PRE
 #cross-references EMBL:X172702; NID:9288927; PID:9288930
 #experimental_source subtype ayw, patient C1000
 #note due to a stop codon between the alternative initiators
 the e antigen precursor cannot be produced

CLASSIFICATION C
KEYWORDS #superfamily hepatitis B virus core antigen
 #core protein
FEATURE 1-29
 30-212 #domain signal sequence #status predicted #label SIG\
 30-212 #product core antigen #status predicted #label CAG\
 179-212 #product e antigen #status predicted #label EAG\
 #domain carboxyl-terminal propeptide #link EAG #status
 predicted #label ECP

SUMMARY #length 212 #molecular-weight 24336 #checksum 770

Query Match 62.3%; Score 1374; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.28e-200;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPYKEFGATVELLSFLPSDFPSVVDLDTASALYREALSPHCSPHHTALRQAI 88
 |||||

OY 112 SMDIDPYKEFGATVELLSFLPSDFPSVVDLDTASALYREALSPHCSPHHTALRQAI 171
 |||||

DB 89 LCMGELMTLATVGVNLEDPASRDLYSVYNTNMGKLFKROLMLFHSCLTGFRETIVIEL 148
 |||||

OY 172 LCMGELMTLATVGVNLEDPASRDLYSVYNTNMGKLFKROLMLFHSCLTGFRETIVIEL 231
 |||||

DB 149 VSGFWIRTPPYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
 |||||

OY 232 VSGFWIRTPPYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 291
 |||||

DB 209 ESQC 212
 |||||

OY 292 ESQC 295

RESULT 5
ENTRY #type complete
TITLE S20750
 e antigen precursor / core antigen - hepatitis B virus
 (subtype ayw, patient CI)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
 #subtype ayw, patient CI
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
 08-Sep-1997

ACCESSIONS
REFERENCE S20750
 S20745

GENETICS #gene
 #residues 1-212 #label LAI
 #cross-references EMBL:X65258; NID:959434; PID:959436
 #experimental_source subtype ayw, patient CI

CLASSIFICATION C
KEYWORDS #superfamily hepatitis B virus core antigen
 #alternative initiators; core protein
FEATURE 1-29
 30-212 #domain signal sequence #status predicted #label SIG\
 30-212 #product core antigen #status predicted #label CAG\
 179-212 #product e antigen #status predicted #label EAG\
 #domain carboxyl-terminal propeptide #link EAG #status
 predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 147

Query Match 62.3%; Score 1373; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 1.88e-200;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPYKEFGATVELLSFLPSDFPSVVDLDTASALYREALSPHCSPHHTALRQAI 88
 |||||

OY 112 SMDIDPYKEFGATVELLSFLPSDFPSVVDLDTASALYREALSPHCSPHHTALRQAI 171
 |||||

DB 89 LCMGELMTLATVGVNLEDPASRDLYSVYNTNMGKLFKROLMLFHSCLTGFRETIVIEL 148
 |||||

OY 172 LCMGELMTLATVGVNLEDPASRDLYSVYNTNMGKLFKROLMLFHSCLTGFRETIVIEL 231
 |||||

DB 149 VSGFWIRTPPYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
 |||||

OY 232 VSGFWIRTPPYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 291
 |||||

DB 209 ESQC 212
 |||||

OY 292 ESQC 295

RESULT 6
ENTRY #type complete
TITLE S53270
 core antigen - hepatitis B virus (isolate patient
 Licheri-2/87)
ALTERNATE_NAMES HBe antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
 #isolate patient Licheri-2/87
 #variety isolate patient Licheri-2/87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

08-Sep-1997

ACCESSIONS S53270

REFERENCE S53112

#authors Lai, M.E.; Mazzeoleni, A.P.; Porru, A.; Balestrieri, A.

#submission submitted to the EMBL Data Library, March 1995

#accession S53270

##molecule_type DNA

##residues 1-183 ##label LAI

##cross-references EMBL:X85314; NID:g736201; PID:g736204

##experimental_source isolate patient Licheri-27/87

##note due to a stop codon between the alternative initiators the e antigen precursor cannot be produced

GENETICS

#gene C

CLASSIFICATION #superfamily hepatitis B virus core antigen

KEYWORDS core protein

SUMMARY #length 183 #molecular-weight 21102 #checksum 2199

Query Match 62.1%; Score 1370; DB 2; Length 183;

Best Local Similarity 98.4%; Pred. No. 5,98e-200;

Matches 180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKEGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALRQAI 60

113 MDIDPKKEGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALRQAI 172

61 CMGDLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETIEYL 120

173 CMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETIEYL 232

Db 121 SFGVWIRTPPAPRPAPNPALSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180

233 SFGVWIRTPPAPRPAPNPALSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 292

Db 181 SQC 183

293 SQC 295

QY

RESULT 7

ENTRY S53216 #type complete

TITLE e antigen precursor / core antigen - hepatitis B virus

ALTERNATE_NAMES HBe antigen precursor / Hbc antigen; pre-C/C antigen

CONTAINS core antigen; e antigen

ORGANISM #formal_name hepatitis B virus; HBV

#variety isolate patient Castag/3

DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

08-Sep-1997

ACCESSIONS S53216

REFERENCE S53112

#authors Lai, M.E.; Mazzeoleni, A.P.; Porru, A.; Balestrieri, A.

#submission submitted to the EMBL Data Library, March 1995

#accession S53216

##molecule_type DNA

##residues 1-212 ##label LAI

##cross-references EMBL:X85293; NID:g736124; PID:g736126

##experimental_source isolate patient Castag/3

GENETICS

#gene C

CLASSIFICATION #superfamily hepatitis B virus core antigen

KEYWORDS alternative initiators; core protein

FEATURE

1-29 #domain signal sequence #status predicted #label SIG\

30-212 #product core antigen #status predicted #label CAG\

30-178 #product e antigen #status predicted #label EAG\

179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24363 #checksum 752

Query Match 62.1%; Score 1370; DB 2; Length 212;

Best Local Similarity 98.9%; Pred. No. 5,98e-200;

Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALRQAI 88

112 SMDIDPKKEGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALRQAI 171

89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETIEYL 148

172 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETIEYL 231

Db 149 VSGVWIRTPPAPRPAPNPALSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208

232 VSGVWIRTPPAPRPAPNPALSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 291

Db 209 ESQC 212

292 ESQC 295

QY

RESULT 8

ENTRY S53272 #type complete

TITLE e antigen precursor / core antigen - hepatitis B virus

ALTERNATE_NAMES HBe antigen precursor / Hbc antigen; pre-C/C antigen

CONTAINS core antigen; e antigen

ORGANISM #formal_name hepatitis B virus; HBV

#variety isolate patient Licheri-3/90

DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

08-Sep-1997

ACCESSIONS S53272

REFERENCE S53112

#authors Lai, M.E.; Mazzeoleni, A.P.; Porru, A.; Balestrieri, A.

#submission submitted to the EMBL Data Library, March 1995

#accession S53272

##molecule_type DNA

##residues 1-212 ##label LAI

##cross-references EMBL:X85315; NID:g736205; PID:g736207

##experimental_source isolate patient Licheri-3/90

GENETICS

#gene C

CLASSIFICATION #superfamily hepatitis B virus core antigen

KEYWORDS alternative initiators; core protein

FEATURE

1-29 #domain signal sequence #status predicted #label SIG\

30-212 #product core antigen #status predicted #label CAG\

30-178 #product e antigen #status predicted #label EAG\

179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24366 #checksum 446

Query Match 62.1%; Score 1370; DB 2; Length 212;

Best Local Similarity 98.9%; Pred. No. 5,98e-200;

Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALRQAI 88

112 SMDIDPKKEGATVELLSFLPSDFPSPVRDLDTASALYREALSEPHSCPHHTALRQAI 171

89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETIEYL 148

172 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETIEYL 231

Db 149 VSGVWIRTPPAPRPAPNPALSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208

232 VSGVWIRTPPAPRPAPNPALSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 291

Db 209 ESQC 212

292 ESQC 295

QY

RESULT 9

ENTRY S53163 #type complete

TITLE e antigen precursor / core antigen - hepatitis B virus

ALTERNATE_NAMES (isolate patient Vittorina/92)
CONTAINS Hbe antigen precursor / Hbc antigen; pre-C/C antigen
#formal_name hepatitis B virus, HBV
#variety
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53163
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Portu, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53163
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85256; NID:g736050; PID:g736052
#experimental_source isolate patient Vittorina/92

GENETICS C
#gene
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24322 #checksum 842

Query Match 62.1%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.9%; Pred. No. 8.80e-200;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALQAI 88
:|||||
QY 112 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALQAI 171
:|||||

Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRTVLEYL 148
:|||||
QY 172 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRTVLEYL 231
:|||||

Db 149 VSFGWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSQSR 208
:|||||
QY 232 VSFGWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSQSR 291
:|||||

Db 209 ESOC 212
:|||||
QY 292 ESOC 295

RESULT 10
ENTRY S20746 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C)
ALTERNATE_NAMES Hbe antigen precursor / Hbc antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997

ACCESSIONS S20746
REFERENCE S20745
#authors Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.;
Portu, A.
#submission submitted to the EMBL Data Library, March 1992
#description Sequence analysis of HBV genomes isolated from patients with
HBsAg negative chronic liver disease.
#accession S20746
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X65257; NID:g59429; PID:g59431
#experimental_source subtype ayw, patient C

GENETICS C
#gene

CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 506

Query Match 62.1%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 8.80e-200;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALQAI 88
:|||||
QY 112 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALQAI 171
:|||||

Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRTVLEYL 148
:|||||
QY 172 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRTVLEYL 231
:|||||

Db 149 VSFGWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSQSR 208
:|||||
QY 232 VSFGWIRTPPAYRPPAPILSTLPETTVARRGRSPRRRTSPRRRSOSPRRRRSQSR 291
:|||||

Db 209 ESOC 212
:|||||
QY 292 ESOC 295

RESULT 11
ENTRY S53225 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Chigline-2/86)
ALTERNATE_NAMES Hbe antigen precursor / Hbc antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53225
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Portu, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53225
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85296; NID:g736137; PID:g736139
#experimental_source isolate patient Chigline-2/86

GENETICS C
#gene
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-212 #product core antigen #status predicted #label CAG\
30-178 #product e antigen #status predicted #label EAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY #length 212 #molecular-weight 24308 #checksum 655

Query Match 62.1%; Score 1369; DB 2; Length 212;
Best Local Similarity 98.4%; Pred. No. 8.80e-200;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALQAI 88
:|||||
QY 112 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALESPHCSPHHTALQAI 171
:|||||

Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRTVLEYL 148
:|||||
QY 172 LCMGELMTLATWGVNLEDPASRDLYSVYNTNGLKFRQLMFHISCLTFGRTVLEYL 231
:|||||

Best Local Similarity 98.9%; Pred. No. 2,80e-199;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 88
:|||||
QY 112 SMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 171
:|||||
Db 89 LCMGELMTLATWGVNLEDPSARDLVSVNTNMGKFRQLMFHISCLTFGRETIVIEL 148
:|||||
QY 172 LCMGELMTLATWGVNLEDPSARDLVSVNTNMGKFRQLMFHISCLTFGRETIVIEL 231
:|||||
Db 149 VSGVWIRTPPAYRPPNAPILTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 208
:|||||
QY 232 VSGVWIRTPPAYRPPNAPILTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 291
:|||||
Db 209 ESOC 212
:|||||
QY 292 ESOC 295

RESULT 15
ENTRY S53169 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Muresu/89)
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Muresu/89
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53169
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53169

##molecule_type DNA
##residues 1-183 ##label LAI
##cross-references EMBL:X85275; NID:g736057; PID:g736060
##experimental_source isolate patient Muresu/89
##note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
SUMMARY #length 183 #molecular_weight 21088 #checksum 1849

Query Match 61.9%; Score 1364; DB 2; Length 183;
Best Local Similarity 98.4%; Pred. No. 6.07e-199;
Matches 180; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 60
:|||||
QY 113 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSEPHHCSPHHTALROAI 172
:|||||
Db 61 CWMGELMTLATWGVNLEDPSARDLVSVNTNMGKFRQLMFHISCLTFGRETIVIEL 120
:|||||
QY 173 CWMGELMTLATWGVNLEDPSARDLVSVNTNMGKFRQLMFHISCLTFGRETIVIEL 232
:|||||
Db 121 SFGVWIRTPPAYRPPNAPILTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 180
:|||||
QY 233 SFGVWIRTPPAYRPPNAPILTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 292
:|||||
Db 181 SOC 183
:|||||
QY 293 SOC 295

Search completed: Thu Dec 16 13:49:08 1999
Job time : 74 secs.

(TM)

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKFEGATVELLSFLPSDFPVSRLDITASALYREALSPHCSPHHTAL 60
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 81012115.
RA LEADBETTER G., MURRAY K.;
RT "Hepatitis B virus genes and their expression in E. coli";
RL NATURE 282:575-579(1979).

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DR EMBL: J02202; G329638; -
DR EMBL: A08967; G411874; -
DR PIR: B93217; NKVLA2.
DR PFAM: PF00906; Hepatitis_core; 1.
KM CORE PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21042 MW; 6EA6B674 CRC32;

Query Match 61.6%; Score 1358; DB 1; Length 211;
Best Local Similarity 95.2%; Pred. No. 2.47e-227;
Matches 179; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 24 LGWMDMDIDPKFEGATVELLSFLPSDFPVSRLDITASALYREALSPHCSPHHTAL 83
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 108 LQSLSMIDPKFEGATVELLSFLPSDFPVSRLDITASALYREALSPHCSPHHTAL 167
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 84 RQALICWGLDITLSTWVGNEDEPTSDLVSVYNTNGLKFRQLMFWHISCLTFRGRTV 143
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 168 RQALICWGLDITLSTWVGNEDEPTSDLVSVYNTNGLKFRQLMFWHISCLTFRGRTV 227
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 144 IEYVSTGVTARTPPAIPAPNPISTLPTETVVRGRGRSPRRRSPRRRSOSPRE 203
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 228 IEYVSTGVTARTPPAIPAPNPISTLPTETVVRGRGRSPRRRSPRRRSOSPRE 287
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 204 TOSRESOC 211
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 288 SOSRESOC 295
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKFEGATVELLSFLPSDFPVSRLDITASALYREALSPHCSPHHTAL 60
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 81012115.
RA LEADBETTER G., MURRAY K.;
RT "Hepatitis B virus genes and their expression in E. coli";
RL NATURE 282:575-579(1979).

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CC or send an email to license@isb-sib.ch).

DR EMBL: J02202; G329638; -
DR EMBL: A08967; G411874; -
DR PIR: B93217; NKVLA2.
DR PFAM: PF00906; Hepatitis_core; 1.
KM CORE PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21042 MW; 6EA6B674 CRC32;

Query Match 61.2%; Score 1349; DB 1; Length 183;
Best Local Similarity 96.7%; Pred. No. 1.34e-225;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDIDPKFEGATVELLSFLPSDFPVSRLDITASALYREALSPHCSPHHTAL 60
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 113 MDIDPKFEGATVELLSFLPSDFPVSRLDITASALYREALSPHCSPHHTAL 172
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 61 CWGLMTLATWGVNEDPASPRLVSVYNTNGLKFRQLMFWHISCLTFRGRTV 120
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 173 CWGLMTLATWGVNEDPASPRLVSVYNTNGLKFRQLMFWHISCLTFRGRTV 232
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 121 SFGWITPPAIPAPNPISTLPTETVVRGRGRSPRRRSPRRRSOSPRE 180
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 233 SFGWITPPAIPAPNPISTLPTETVVRGRGRSPRRRSPRRRSOSPRE 292
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 181 SOC 183
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

Db 293 SOC 295
AC P3147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN
OS HEPATITIS B VIRUS (SUBTYPE ADYN).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes";

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RL J. GEN. VIROL. 69:2575-2583(1988).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D00330; -. NOT_ANNOTATED_CDS.
DR PIR: B28925; NKVLJ2.
DR PFAM: PF00906; Hepatitis_core; 1.
DR CORE PROTEIN: REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 115B9E3 CRC32;

Query Match
Best Local Similarity 96.2%; Pred. No. 4,26e-223;
Matches 176; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 1 MDIDYKEFGASVELSLSPDFFPSVRDLDTASALYREALSEPHCSPHHTALROAIL 60
    |||
QY 113 MDIDYKEFGATVELSLSPDFFPSVRDLDTASALYREALSEPHCSPHHTALROAIL 172
    |||
Db 61 CWGELMTATWGVNLEDPASRELVSYNVMGLKIRQLMFHISCLTFGRETLEYLY 120
    |||
QY 173 CWGELMTATWGVNLEDPASRELVSYNVMGLKIRQLMFHISCLTFGRETLEYLY 232
    |||
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
    |||
QY 233 SFGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 292
    |||
Db 181 SOC 183
    |||
QY 293 SOC 295

RESULT 5
ID CORA_HPBV4 STANDARD: PRT: 183 AA.
AC P03150; P03151;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C
OS HEPATITIS B VIRUS (SUBTYPE ADR), HEPATITIS B VIRUS (SUBTYPE ADR4),
OS AND HEPATITIS B VIRUS (SUBTYPE ADM / STRAIN INDONESIA/PIDM420).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ADR:
RX MEDLINE: 83168919.
RX ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA: subtype adr and adm."
RL 7 NUCLEIC ACIDS RES. 11:1747-1757(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-ADR4:
RX MEDLINE: 83246570.
RX FUJUYAMA A., MIYANOHARA A., NOZAKI C., YONEYAMA T., OHTOMO N.,
RA MATSUBARA K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr."
RL NUCLEIC ACIDS RES. 11:4601-4610(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-ADM:
RX MEDLINE: 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MATSUMI M.;
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RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. GEN. VIROL. 69:2575-2583(1988).
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CC -----
DR EMBL: V00867; -. NOT_ANNOTATED_CDS.
DR EMBL: X01587; G59407; -.
DR EMBL: D00331; -. NOT_ANNOTATED_CDS.
DR PIR: A93480; NKVLJ3.
DR PIR: B28925; NKVLJ2.
DR PIR: B28925; NKVLJ3.
DR PFAM: PF00906; Hepatitis_core; 1.
DR CORE PROTEIN: REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21095 MW; D2E185B9 CRC32;

Query Match
Best Local Similarity 95.6%; Score 1334; DB 1; Length 183;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 MDIDYKEFGASVELSLSPDFFPSVRDLDTASALYREALSEPHCSPHHTALROAIL 60
    |||
QY 113 MDIDYKEFGATVELSLSPDFFPSVRDLDTASALYREALSEPHCSPHHTALROAIL 172
    |||
Db 61 CWGELMTATWGVNLEDPASRELVSYNVMGLKIRQLMFHISCLTFGRETLEYLY 120
    |||
QY 173 CWGELMTATWGVNLEDPASRELVSYNVMGLKIRQLMFHISCLTFGRETLEYLY 232
    |||
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
    |||
QY 233 SFGWIRTPPAYRPPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 292
    |||
Db 181 SOC 183
    |||
QY 293 SOC 295

RESULT 6
ID CORA_HPBV4 STANDARD: PRT: 183 AA.
AC P17391;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
OS HEPATITIS B VIRUS (SUBTYPE ADM / STRAIN JAPAN/PJDM233).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ADM:
RX MEDLINE: 89010694.
RX OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MATSUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes."
RL J. GEN. VIROL. 69:2575-2583(1988).
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CC -----
DR EMBL: D00329; -. NOT_ANNOTATED_CDS.
DR PIR: A28925; NKVLJ1.
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DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN: REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SO SEQUENCE 183 AA; 21224 MW; F6B348B6 CRC32;
Query Match 60.0%; Score 1322; DB 1; Length 183;
Best Local Similarity 96.2%; Pred. No. 2,11e-220;
Matches 176; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 MDIDPYKFGATVLLSFLSDFFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
113 MDIDPYKFGATVLLSFLSDFFPSVRDLDTASALYREALSPHCSPHHTALROAIL 172
61 CWGELMTLATVGNLDPASRDLYVYVNTNMGLKIRQLMWFHISCLTFGRVLEYLY 120
173 CWGELMTLATVGNLDPASRDLYVYVNTNMGLKIRQLMWFHISCLTFGRVLEYLY 232
121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSPRE 180
233 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSPRE 292
181 SOC 183
293 SOC 295

RESULT 7
ID CORA_HPBVT STANDARD; PRT; 185 AA.
AC P03149;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 83168919.
RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
DNA; subtype adr and adw.";
RL NUCLEIC ACIDS RES. 11:1747-1757(1983).
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CC
CC EMBL: V00866; NOT_ANNOTATED_CDS.
DR PIR: C93460; NKVL46.
DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN: REPEAT.
FT REPEAT 164 171
FT REPEAT 172 179
SO SEQUENCE 185 AA; 21394 MW; 791E0381 CRC32;
Query Match 59.9%; Score 1321; DB 1; Length 185;
Best Local Similarity 96.2%; Pred. No. 3,29e-220;
Matches 178; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Db 1 MDIDPYKFGATVLLSFLSDFFPSVRDLDTASALYREALSPHCSPHHTALROAIL 60
113 MDIDPYKFGATVLLSFLSDFFPSVRDLDTASALYREALSPHCSPHHTALROAIL 172
61 CWGELMTLATVGNLDPASRDLYVYVNTNMGLKIRQLMWFHISCLTFGRVLEYLY 120
173 CWGELMTLATVGNLDPASRDLYVYVNTNMGLKIRQLMWFHISCLTFGRVLEYLY 232

Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSPRE 180
233 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSPRE 290
181 RESOC 185
291 RESOC 295

RESULT 8
ID CORA_HPBVT STANDARD; PRT; 195 AA.
AC P29178;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW2 VARIANT SF).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 90169850.
RA BHAT R.A., ULRICH P.P., VYAS G.N.;
RT "Molecular characterization of a new variant of hepatitis B virus in
a persistently infected homosexual man.";
RL HEPATOLOGY 11:271-276(1990).
DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN: REPEAT.
FT REPEAT 174 181
FT REPEAT 182 189
SO SEQUENCE 195 AA; 22461 MW; AF3DB5F3 CRC32;
Query Match 59.6%; Score 1314; DB 1; Length 195;
Best Local Similarity 93.5%; Pred. No. 7,31e-219;
Matches 173; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 11 FGDLIDPYKFGATVLLSFLSDFFPSVRDLDTASALYREALSPHCSPHHTALROA 70
111 LSMDIDPYKFGATVLLSFLSDFFPSVRDLDTASALYREALSPHCSPHHTALROA 170
71 ILGWELMTLATVGNLDPASRDLYVYVNTNMGLKIRQLMWFHISCLTFGRVLEYLY 130
171 ILGWELMTLATVGNLDPASRDLYVYVNTNMGLKIRQLMWFHISCLTFGRVLEYLY 230
131 LVSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSPRE 190
231 LVSEGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTPSPRRRSQSPRRRSQSPRE 290
191 RESOC 195
291 RESOC 295

RESULT 9
ID CORA_HPBVT STANDARD; PRT; 212 AA.
AC O05495;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE W4B).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 93346870.
RA NAUMANN H., SCHAEFER S., YOSHIDA C.F.T., GASPAR A.M.C., REPP R.,
RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
that expresses HBV surface antigen subtype adw4.";
RL J. GEN. VIROL. 74:1627-1632(1993).
CC


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OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN 991).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA KOEHEL H.G., SCHUELER A., LOTTMANN S., THOMSEN R.;
RA SUBMITTED (FEB-1990) TO EMBL/GENEBANK/DBD DATA BANKS.
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CC -----
DR EMBL: X51970; G60433; -
DR PIR: S10381; NKVLKS.
DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA: 24722 MW: 786CD048 CRC32;

Query Match 59.1%; Score 1304; DB 1; Length 214;
Best Local Similarity 95.2%; Pred. No. 6.14e-217;
Matches 177; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

Db 29 GMDIDPKYKFGATVLLSLPDSFPFSDVLDLDTASALREALSEPHHTRALROI 88
QY :|||||
Db 112 SMIDPKYKFGATVLLSLPDSFPFSDVLDLDTASALREALSEPHHTRALROI 171
QY :|||||
Db 89 LCMGELMTLATWGNLLEDPASRDVLYVNTNMGLKIRQLMFRISYLTFGRETVLEYL 148
QY :|||||
Db 172 LCMGELMTLATWGNLLEDPASRDVLYVNTNMGLKIRQLMFRISYLTFGRETVLEYL 231
QY :|||||
Db 149 VSPGWIRPPAPRPAPNAPILSTLPETVYVRRRGRSRRRRSPRRRSQ 208
QY :|||||
Db 232 VSPGWIRPPAPRPAPNAPILSTLPETVYVRRRGRSRRRRSPRRRSQ 289
QY :|||||
Db 209 SRESOC 214
QY :|||||
QY 290 SRESOC 295

RESULT 13
ID CORA_MHV1 STANDARD: PRT: 188 AA.
AC P03152;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 1 (MHV 1),
OS WOODCHUCK HEPATITIS VIRUS 7 (MHV 7),
OS WOODCHUCK HEPATITIS VIRUS 59 (MHV 59), AND
OS WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE) (MHV 8).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA SPECIES=WOODCHUCK HEPATITIS VIRUS 1;
RX MEDLINE: 82216969.
RA GALIBERT F., CHEN T.N., MANDART E.;
RA "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RA comparison with the hepatitis B virus sequence.";
RL J. VIROL. 41:51-65(1982).
RN [2]
RP SEQUENCE FROM N.A.
RA SPECIES=WOODCHUCK HEPATITIS VIRUS 7, AND WOODCHUCK HEPATITIS VIRUS 59;
RX MEDLINE: 88101359.
RA COHEN J.I., MILLER R.H., ROSENBLUM B., DENNISTON K., GERIN J.L.,
RA PURELL R.H.;
RA "Sequence comparison of woodchuck hepatitis virus replicative forms
RA shows conservation of the genome.";

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RL VIROLOGY 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE);
RX MEDLINE: 89184524.
RA GIRONES R., COTE P.J., HORNEBUCKLE W.E., TENNANT B.C., GERIN J.L.,
RA PURELL R.H., MILLER R.H.;
RA "Complete nucleotide sequence of a molecular clone of woodchuck
RA hepatitis virus that is infectious in the natural host.";
RL PROC. NATL. ACAD. SCI. U.S.A. 86:1846-1849(1989).
RL -----
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CC -----
DR EMBL: J02442; G336129; -
DR EMBL: M18752; G336140; -
DR EMBL: M19183; G336145; -
DR EMBL: J04514; G336149; -
DR PIR: A03713; NKVLC.
DR PIR: C32397; NKVLC.
DR PIR: C32397; NKVLC4.
DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA: 21693 MW: A667DB27 CRC32;

Query Match 42.5%; Score 938; DB 1; Length 188;
Best Local Similarity 67.0%; Pred. No. 5.57e-147;
Matches 126; Conservative 25; Mismatches 32; Indels 5; Gaps 1;

Db 1 MDIDPKYKFGATVLLSLPDSFPFSDVLDLDTASALREALSEPHHTRALROI 60
QY :|||||
QY 113 MDIDPKYKFGATVLLSLPDSFPFSDVLDLDTASALREALSEPHHTRALROI 172
QY :|||||
Db 61 CMDELTKLIAMMSNITSEQVRTIIVNHNVDWGLKIVQSLMFLHSCITFGHTQOEY 120
QY :|||||
QY 173 CMGELMTLATWGNLLEDPASRDVLYVNTNMGLKIRQLMFRISYLTFGRETVLEYL 232
QY :|||||
Db 121 SPGWIRPPAPRPAPNAPILSTLPETVYVRRRGRSRRRRSPRRRSQ 180
QY :|||||
QY 233 SPGWIRPPAPRPAPNAPILSTLPETVYVRRRGRSRRRRSPRRRSQ 287
QY :|||||
Db 181 SOSPSANC 188
QY :|||||
QY 288 SOSRESOC 295

RESULT 14
ID CORA_HPBGS STANDARD: PRT: 217 AA.
AC P03153;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS GROUND SQUIRREL HEPATITIS VIRUS (GSVH).
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA SEEGER C., GANEM D., VARMS H.E.;
RA "Nucleotide sequence of an infectious molecularly cloned genome of
RA ground squirrel hepatitis virus.";
RL J. VIROL. 51:367-375(1984).
CC -----
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DR EMBL: K02715; G325401; -.
DR PIR: A03715; NKVL5.
DR PFAM: PF00906; Hepatitis_core; 1.
KM CORE PROTEIN; REPEAT.
FT REPEAT 196 203
FT REPEAT 204 211
SQ SEQUENCE 217 AA; 25189 MW; B70A00B1 CRC32;

Query Match 42.4%; Score 934; DB 1; Length 217;
Best Local Similarity 68.1%; Pred. No. 3.20e-146;
Matches 128; Conservative 22; Mismatches 32; Indels 6; Gaps 2;

Db 31 MDIDPYKEFGSSVQLNLFPLDFFPDNALVDYTAALYEELTGREHCSPHHTAIRQALV 90
113 MDIDPYKEFGATVELLSFLPSDFPSVRLDITASALYREALSPHCSPHHTAIRQAIL 172
QY 91 CWDELTKLIAMSSNITSEGVRTIIVHNDTWGLKVRQSLMFLSCLTFGQHTVOEFLV 149
173 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLMFLHISCLTFGRETIVIEYLV 232
Db 150 SFVWIRTAPYRPPNAPILSTLPEHTVIRRGAGARASRRRTSPRRRSQSPRRRR 209
QY 233 SFGVWIRTPPAYRPPNAPILSTLPEHTVIRRGAGARASRRRTSPRRRSQSPRRRR 287
Db 210 QSPSANC 217
QY 288 QSRRESQC 295

RESULT 15
ID CORA_MHV8 STANDARD; PRT; 187 AA.
AC P06433;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 8 (MHV 8).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86062931.
RA KODAMA K., OGASAWARA N., YOSHIKAWA H., MURAKAMI S.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT evolutionary relationship between hepadnaviruses.";
RL J. VIROL. 56:978-986(1985).

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DR EMBL: M11082; G336135; -.
DR PIR: A03714; NKVL2.
DR PFAM: PF00906; Hepatitis_core; 1.
KM CORE PROTEIN; REPEAT.
FT REPEAT 166 173
FT REPEAT 174 181
SQ SEQUENCE 187 AA; 21579 MW; A1C354F3 CRC32;

Query Match 42.3%; Score 933; DB 1; Length 187;
Best Local Similarity 66.3%; Pred. No. 4.94e-146;
Matches 124; Conservative 26; Mismatches 33; Indels 4; Gaps 2;

Db 1 MDIDPYKEFGSSVQLNLFPLDFFPDNALVDYTAALYEELTGREHCSPHHTAIRQALV 60
113 MDIDPYKEFGATVELLSFLPSDFPSVRLDITASALYREALSPHCSPHHTAIRQAIL 172
QY 61 CWDELTKLIAMSSNITSEGVRTIIVHNDTWGLKVRQSLMFLSCLTFGQHTVOEFLV 120
173 CWGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLMFLHISCLTFGRETIVIEYLV 232
Db 121 SFVWIRTAPYRPPNAPILSTLPEHTVIRRGAGARASRRRTSPRRRSQSPRRRR 180
QY 233 SFGVWIRTPPAYRPPNAPILSTLPEHTVIRRGAGARASRRRTSPRRRSQSPRRRR 288
Db 181 QSPSANC 187
QY 289 QSRRESQC 295

Search completed: Thu Dec 16 13:49:59 1999
Job time : 33 secs.

Query Match 62.4%; Score 1375; DB 14; Length 212;
Best Local Similarity 99.5%; Pred. No. 2,79e-219;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
QY 112 SMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 171
DB 89 LCMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFHISCLTFGRETIVIEL 148
QY 172 LCMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFHISCLTFGRETIVIEL 231
DB 149 VSGVWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSR 208
QY 232 VSGVWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSR 291
DB 209 ESQC 212
QY 292 ESQC 295

RESULT 2
ID 089437 PRELIMINARY; PRT; 183 AA.
AC 089437;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (CASTAA 2).
GN CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RN RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTAA-2/87;
RC LAI M.E., MAZZOLENTI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN (2)
RN RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RC KARAYIANNIS P.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN (3)
RN RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85289; G736113; -;
DR EMBL: X80925; E198085; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SO SEQUENCE 183 AA; 21102 MW; 0C504D47 CRC32;

Query Match 62.3%; Score 1373; DB 14; Length 183;
Best Local Similarity 99.5%; Pred. No. 6,48e-219;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
QY 113 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 172
DB 61 CMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFHISCLTFGRETIVIEL 120
QY 173 CMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFHISCLTFGRETIVIEL 232
DB 121 SFGVWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSR 180
QY 233 SFGVWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSR 292
DB 181 SOC 183
QY 293 SOC 295

RESULT 3

ID 068008 PRELIMINARY; PRT; 183 AA.
AC 068008;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (FERACCTI 1).
GN CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RN RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT FERRACCTI-1/89;
RC LAI M.E., MAZZOLENTI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85284; G736098; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SO SEQUENCE 183 AA; 21102 MW; BB9DAFBB CRC32;

Query Match 62.3%; Score 1373; DB 14; Length 183;
Best Local Similarity 99.5%; Pred. No. 6,48e-219;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 1 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 60
QY 113 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 172
DB 61 CMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFHISCLTFGRETIVIEL 120
QY 173 CMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFHISCLTFGRETIVIEL 232
DB 121 SFGVWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSR 180
QY 233 SFGVWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSR 292
DB 181 SOC 183
QY 293 SOC 295

RESULT 4
ID 068020 PRELIMINARY; PRT; 212 AA.
AC 068020;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN (1)
RN RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTAG-1/85;
RC LAI M.E., MAZZOLENTI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85291; G736119; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SO SEQUENCE 212 AA; 24336 MW; E0E4C243 CRC32;

Query Match 62.3%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 4,25e-219;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 88
QY 112 SMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALRQAI 171
DB 89 LCMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFHISCLTFGRETIVIEL 148
QY 172 LCMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFHISCLTFGRETIVIEL 231
DB 149 VSGVWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSR 208
QY 232 VSGVWIRTPPAYRPPNAPILSTLPEITVVRGRGSPRRRTSPRRRSQSPRRRSQSR 291

Db 209 ESQC 212
1111
QY 292 ESQC 295

RESULT 5
ID 089597 PRELIMINARY; PRT; 212 AA.
AC 089597;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HEPAG.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN-SUB-TYPE AYM.
RA MEDLINE; 94079539.
RA PREISLER-ADAMS S., SCHLAYER M.J., PETERS T., HETTLER F., GEROK W.,
RA RASENACK J.;
RT "Sequence analysis of hepatitis B virus DNA in immunologically
RT negative infection";
RL ARCH. VIROL. 133:385-396(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AYM;
RA KARAYIANNIS P.;
RN SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-AYM;
RA KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X172702; G288830; -;
DR EMBL: X80925; E198084; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24336 MW; 575D20BF CRC32;

Query Match 62.3%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 4.25e-219;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHNTALROAI 88
:|||||
QY 112 SMDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHNTALROAI 171

Db 89 LCMGELMTLATWGVNLEDPASRDVLSYVNTNNGKLFROLMFHISCLTFGRETVEYL 148
:|||||
QY 172 LCMGELMTLATWGVNLEDPASRDVLSYVNTNNGKLFROLMFHISCLTFGRETVEYL 231

Db 149 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||
QY 232 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291

Db 209 ESQC 212
1111
QY 292 ESQC 295

RESULT 6
ID 067876 PRELIMINARY; PRT; 212 AA.
AC 067876;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE C/C ORF.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CT, HBV SUBTYPE AYM;
RA LAI M.E., MAZOLENTI A.P., BALESTRIERI A., MELIS A., PORRU A.;

RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65258; G59436; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24348 MW; 6ED741BE CRC32;

Query Match 62.3%; Score 1373; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 6.48e-219;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHNTALROAI 88
:|||||
QY 112 SMDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHNTALROAI 171

Db 89 LCMGELMTLATWGVNLEDPASRDVLSYVNTNNGKLFROLMFHISCLTFGRETVEYL 148
:|||||
QY 172 LCMGELMTLATWGVNLEDPASRDVLSYVNTNNGKLFROLMFHISCLTFGRETVEYL 231

Db 149 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||
QY 232 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291

Db 209 ESQC 212
1111
QY 292 ESQC 295

RESULT 7
ID 011884 PRELIMINARY; PRT; 212 AA.
AC 011884;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN PRECURSOR.
OC HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA RAO B.S., CASEY J.L., RINAUDO J.S., KORBA B.E.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U95551; G2182120; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24360 MW; 73AC92DB CRC32;

Query Match 62.2%; Score 1372; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 9.87e-219;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHNTALROAI 88
:|||||
QY 112 SMDIDPYKEFGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHNTALROAI 171

Db 89 LCMGELMTLATWGVNLEDPASRDVLSYVNTNNGKLFROLMFHISCLTFGRETVEYL 148
:|||||
QY 172 LCMGELMTLATWGVNLEDPASRDVLSYVNTNNGKLFROLMFHISCLTFGRETVEYL 231

Db 149 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
:|||||
QY 232 VSEGVWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291

Db 209 ESQC 212
1111
QY 292 ESQC 295

RESULT 8
ID 068066 PRELIMINARY; PRT; 183 AA.
AC 068066;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (LICHERI 2).
OS HEPATITIS B VIRUS.

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LICHERI-2'87;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85314; G736204; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 183 AA; 21102 MW; 6F38A3B CRC32;

Query Match 62.1%; Score 1370; DB 14; Length 183;
Best Local Similarity 98.4%; Pred. No. 2.29e-218;
Matches 180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKKEGATVELLSFLPSDFPVSVDLDTASALYREALSEPHSCSPHHTALROAI 60
113 MDIDPKKEGATVELLSFLPSDFPVSVDLDTASALYREALSEPHSCSPHHTALROAI 172
Db 61 CWDMLTLATWGVNLEDPASRDLYSVYNTNMGKLFQRLMFHISCLTFGRETYEYL 120
173 CWDMLTLATWGVNLEDPASRDLYSVYNTNMGKLFQRLMFHISCLTFGRETYEYL 232
Db 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
233 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 292
Db 181 SOC 183
293 SOC 295

RESULT 9
ID 068068 PRELIMINARY; PRT; 212 AA.

AC 068068;
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LICHERI-3'90;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85315; G736207; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24366 MW; AB227A9B CRC32;

Query Match 62.1%; Score 1370; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 2.29e-218;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPVSVDLDTASALYREALSEPHSCSPHHTALROAI 88
112 SMDIDPKKEGATVELLSFLPSDFPVSVDLDTASALYREALSEPHSCSPHHTALROAI 171
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFQRLMFHISCLTFGRETYEYL 148
172 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFQRLMFHISCLTFGRETYEYL 231
Db 149 VSRGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
232 VSRGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 291
Db 209 ESOC 212
292 ESOC 295

RESULT 10
ID 068025 PRELIMINARY; PRT; 212 AA.

AC 068025;
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTAG'3;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85293; G736126; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;

Query Match 62.1%; Score 1370; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 2.29e-218;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPVSVDLDTASALYREALSEPHSCSPHHTALROAI 88
112 SMDIDPKKEGATVELLSFLPSDFPVSVDLDTASALYREALSEPHSCSPHHTALROAI 171
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFQRLMFHISCLTFGRETYEYL 148
172 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFQRLMFHISCLTFGRETYEYL 231
Db 149 VSRGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
232 VSRGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 291
Db 209 ESOC 212
292 ESOC 295

RESULT 11
ID 067872 PRELIMINARY; PRT; 212 AA.

AC 067872;
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
DE PRE C/C ORF.
GN HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT C, HBSAG POSITIVE, HBV SUBTYPE ATW;
RA LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A., PORRU A.;
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65257; G59431; -.
PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24348 MW; A6BD9DA1 CRC32;

Query Match 62.1%; Score 1369; DB 14; Length 212;
Best Local Similarity 98.4%; Pred. No. 3.49e-218;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPVSVDLDTASALYREALSEPHSCSPHHTALROAI 88
112 SMDIDPKKEGATVELLSFLPSDFPVSVDLDTASALYREALSEPHSCSPHHTALROAI 171
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFQRLMFHISCLTFGRETYEYL 148
172 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFQRLMFHISCLTFGRETYEYL 231
Db 149 VSRGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
232 VSRGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSQSR 291
Db 209 ESOC 212

```
QY 292 ESOC 295
|||||
RESULT 12
ID 067984 PRELIMINARY; PRT; 212 AA.
AC 067984;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT VITTORINA'92;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85256; G736052; -.
PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24322 MW; 83D9780B CRC32;

Query Match
Best Local Similarity 98.9%; Score 1369; DB 14; Length 212;
Pred. No. 3.49e-218;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||
QY 112 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 171
|||||
Db 89 LCMGELMTLATWGVNEDPASRDVLSYVNTNMGKLFROLMHISCLTFRGTVEYL 148
|||||
QY 172 LCMGELMTLATWGVNEDPASRDVLSYVNTNMGKLFROLMHISCLTFRGTVEYL 231
|||||
Db 149 VSGFWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
|||||
QY 232 VSGFWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291
|||||
Db 209 ESOC 212
|||||
QY 292 ESOC 295

RESULT 13
ID 068032 PRELIMINARY; PRT; 212 AA.
AC 068032;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CHIGINE-2'86;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85296; G736139; -.
PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24308 MW; 69D87B53 CRC32;

Query Match
Best Local Similarity 98.4%; Score 1369; DB 14; Length 212;
Pred. No. 3.49e-218;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||
QY 112 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 171
|||||
Db 89 LCMGELMTLATWGVNEDPASRDVLSYVNTNMGKLFROLMHISCLTFRGTVEYL 148
|||||
QY 172 LCMGELMTLATWGVNEDPASRDVLSYVNTNMGKLFROLMHISCLTFRGTVEYL 231
|||||
Db 149 VSGFWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
|||||
QY 232 VSGFWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291
|||||
Db 209 ESOC 212
|||||
QY 292 ESOC 295
```

```
QY 172 LCMGELMTLATWGVNEDPASRDVLSYVNTNMGKLFROLMHISCLTFRGTVEYL 231
|||||
Db 149 VSGFWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
|||||
QY 232 VSGFWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291
|||||
Db 209 ESOC 212
|||||
QY 292 ESOC 295

RESULT 14
ID 068010 PRELIMINARY; PRT; 212 AA.
AC 068010;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT FERRACUTI-2'90;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85285; G736100; -.
PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24292 MW; 04A4D12D CRC32;

Query Match
Best Local Similarity 98.0%; Score 1368; DB 14; Length 212;
Pred. No. 5.32e-218;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
:|||||
QY 112 SMDIDPKFEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 171
|||||
Db 89 LCMGELMTLATWGVNEDPASRDVLSYVNTNMGKLFROLMHISCLTFRGTVEYL 148
|||||
QY 172 LCMGELMTLATWGVNEDPASRDVLSYVNTNMGKLFROLMHISCLTFRGTVEYL 231
|||||
Db 149 VSGFWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 208
|||||
QY 232 VSGFWIRTPPAYRPPNAPILSTLPTTVVRRGRSPRRRTSPRRRSOSPRRRRSOSR 291
|||||
Db 209 ESOC 212
|||||
QY 292 ESOC 295

RESULT 15
ID 068070 PRELIMINARY; PRT; 212 AA.
AC 068070;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT GORDO'84;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85316; G736210; -.
PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24376 MW; 80F52D0F CRC32;

Query Match
Best Local Similarity 98.0%; Score 1366; DB 14; Length 212;
Pred. No. 1.24e-217;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Db 29 GMDIDPYKEFGATVELLSFLPSDFPFPSVRDLDTASALYREALESPHCSPHHTALROAI 88
:|||||
QY 112 SMDIDPYKEFGATVELLSFLPSDFPFPSVRDLDTASALYREALESPHCSPHHTALROAI 171
|||||
Db 89 LCMGELMTLATWGVNLEDPASRDVSYVNTNMGKFRQLMFHISCLTFGRETVEYL 148
|||||
QY 172 LCMGELMTLATWGVNLEDPASRDVSYVNTNMGKFRQLMFHISCLTFGRETVEYL 231
|||||
Db 149 VSFQWIRTPPAYRPPNAPITLTPETTIVRRGRSPRRTPSPRRRSQSPRRRSQSR 208
|||||
QY 232 VSFQWIRTPPAYRPPNAPITLTPETTIVRRGRSPRRTPSPRRRSQSPRRRSQSR 291
|||||
Db 209 ESQC 212
|||||
QY 292 ESQC 295
```

Search completed: Thu Dec 16 13:52:01 1999
Job time : 104 secs.

US3890-1-38183
MDIDPYKEFGATVELLSFLPSDFPVSVDLDTASALYREALSEPHCSPHHTALROAILCNGELMTLAT
WGVNLEDPAASDLVSVNEITRDGFLLOMDGFEPEHLVDFLOSLMDIDPYKEFGATVELLSFLP
SDFPVSVDLDTASALYREALSEPHCSPHHTALROAILCNGELMTLATWGVNLEDPAASDLVSVN
TNMGLKFRQLMTFHISCTIFGCREVIELVSGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRT
PSPRRRSOSFRRRSQRESOC1

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 16 13:32:26 1999; Maspar time 13.80 Seconds

Tabular output not generated. 467.015 Million cell updates/sec

Title: >US3890-1-38183
 Description: (1-303) from us3890-1-38183.pep
 Perfect Score: 2263
 Sequence: 1 MDIDPKKFGATVELLSFLP.....RRRSQSPRRRSQSRNSQC 303

Scoring table: PAM 150
 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 33.516; Variance 173.687; scale 0.193

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1375	60.8	194	32	W50242	Hepatitis B virus pre
2	1375	60.8	212	32	W50250	Hepatitis B virus pre
3	1375	60.8	346	5	R27473	S12/core protein.
4	1363	60.2	184	1	P80959	Hepatitis B virus sub
5	1359	60.1	193	32	W50241	Hepatitis B virus pre
6	1358	60.0	183	32	W50251	Hepatitis B virus p21
7	1353	59.8	183	20	W09044	Hepatitis B virus cor
8	1349	59.6	183	1	R05635	Hepatitis B antigen.
9	1344	59.4	183	5	P00041	Sequence of core anti
10	1338	59.1	184	5	W09048	Plasmid pHBV DN AA en
11	1337	59.1	208	8	R40804	Sequence of core anti
12	1337	59.0	196	8	R40806	Hepatitis B core / pV
13	1336	58.9	183	4	P40311	Hepatitis B virus core
14	1334	58.9	183	8	R40805	Hepatitis B core prot
15	1334	58.9	183	13	R68868	Hepatitis B virus pol
16	1334	58.9	183	13	R68868	Hepatitis B virus pol

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
17	1334	58.9	183	12	R62869	Hepatitis B virus cor
18	1333	58.9	198	8	R40807	Hepatitis B core / IL
19	1328	58.7	293	10	R55286	Presl full length cor
20	1325	58.6	183	13	R68866	Hepatitis B virus pol
21	1325	58.6	214	1	P90702	Deduced amino acid se
22	1325	58.6	289	20	W09049	Plasmid pHBV DN BB en
23	1324	58.5	185	6	R30861	Hepatitis B core anti
24	1324	58.5	185	10	R55284	Deduced sequence of f
25	1324	58.5	185	6	R30780	Native HBcAg protein.
26	1324	58.5	185	6	R31025	Core antigen of HBV.
27	1321	58.4	185	26	P30061	Hepatitis B virus pol
28	1320	58.3	183	13	R68869	Altered HBcAg protein
29	1317	58.2	185	6	R30781	Altered HBcAg protein
30	1317	58.2	185	6	R31026	Altered HBcAg protein
31	1314	58.1	183	13	R68867	Hepatitis B virus pol
32	1313	58.0	183	13	R68870	Hepatitis B virus pol
33	1311	57.9	185	6	R30784	Altered HBcAg protein
34	1311	57.9	185	6	R31029	Altered HBcAg protein
35	1311	57.9	185	6	R30865	Modified hepatitis B
36	1309	57.8	185	6	R30862	Hepatitis B core anti
37	1308	57.8	185	6	R31028	Altered HBcAg protein
38	1308	57.8	185	6	R30783	Modified hepatitis B
39	1308	57.8	185	6	R30864	Hepatitis B core anti
40	1303	57.6	214	1	P80961	HBV core antigen enco
41	1302	57.5	203	1	P82872	HBcAg/Beta-Gal fusion
42	1287	56.9	198	32	W50252	Hepatitis B virus pre
43	1263	55.8	183	17	R98878	Hepatitis B virus E a
44	1259	55.6	183	17	R98883	Hepatitis B virus E a
45	1258	55.6	183	17	R98884	Hepatitis B virus E a

ALIGNMENTS

RESULT 1
 ID W50242 standard; Protein; 194 AA.
 AC W50242;
 DT 28-SEP-1998 (first entry)
 DE Hepatitis B virus precore p22 polypeptide Met-p22.
 KM Viral replication; inhibitor: HBV; nucleocapsid; gene therapy;
 KW hepatocyte; liver; Met-p22.
 OS Hepatitis B virus.
 SS Synthetic.
 FH Key
 FT Protein
 FT 2..194
 FT Label- p22
 FM W0909649-A1.
 FM 12-MAR-1998.
 PF 03-SEP-1997; U15500.
 PR 03-SEP-1996; US-025370.
 PA (GENO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR;
 DR WPI: 98-193325/17
 PT DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus
 PS Claim 11: Page 40: 60pp; English.
 CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
 CC protein with an added N-terminal Met residue. p22 is produced by
 CC elimination of the 19-amino acid leader peptide from the 25 kDa
 CC full-length HBV precore protein (see W50250). Evidence is provided
 CC that HBV replication is inhibited in the presence of high levels of
 CC HBV precore or precore-related proteins. These proteins can be
 CC incorporated into HBV nucleocapsids along with the p21 core protein
 CC (see W50251), which is the usual nucleocapsid component, and
 CC thereby render the nucleocapsids deficient in encapsidating HBV
 CC pregenomic RNA. Thus, over-expression of the precore proteins, or
 CC certain variants of them, leads to transdominant inhibition of HBV
 CC replication. Suitable inhibitory proteins include p25 (see W50250),
 CC p22, Met-p22, p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
 CC (see W50238). Heterologous peptides (see W50244-49) may be
 CC inserted into the p22 and Met-p22 polypeptides. The inhibitory
 CC proteins can be produced by recombinant methods using claimed
 CC expression vectors and host cells. They can be provided exogenously

CC to the target cells for use in inhibiting HBV replication.
 CC Alternatively, a nucleic acid construct that directs overexpression
 CC of an inhibitory protein in target cells is used for the gene
 CC therapy of HBV infection.
 SQ Sequence 194 AA;

Query Match 60.8%; Score 1375; DB 32; Length 194;
 Best Local Similarity 99.5%; Pred. No. 6.72e-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 11 gmididykefgatvellsfipstfifsvrldltaasalyrealsepncsphtalrgai 70
 :|||||
 QY 120 SMDIDPYKEGATVELLSFIPSDFFPSVRDLDTASALYREALSEPHCSPHHTALROAI 179
 Db 71 lwcgelmrlatwgvnlcdpasrdlvsvyntmglkfifqllwfhlscltfgretvieyl 130
 :|||||
 QY 180 LCGELMTLATWGVNLCDPASRDLVSVYNTMGLKFRQLMFIHISCLTFGRVTIEYL 239
 Db 131 vsfgvwlrtppayrppnapilstlpettvrrrgsprrrrrsgsprrrrrsgsr 190
 :|||||
 QY 240 VSRGVWIRTPPAYRPPNAPILSTLPETTVRRRGSRPRRRTPSPRRRSQSRRRSQSR 299
 Db 191 esgc 194
 :||||
 QY 300 ESQC 303

RESULT 2

ID W50250 standard: Protein; 212 AA.
 AC W50250;
 DT 28-SEP-1998 (first entry)
 DE Hepatitis B virus precore p25 polypeptide.
 KM Hepatitis B virus; inhibitor; HBV; nucleocapsid; gene therapy;
 OS Hepatocyte; liver; p25 protein.
 KM Hepatitis B virus.
 PN W09809649-A1.
 PD 12-MAR-1998.
 PF 03-SEP-1997; 015500.
 PR 03-SEP-1996; US-025370.
 PA (GHEO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR;
 DR WPI: 98-193325/17.
 PT DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus
 PS Claim 15; Page 35; 60pp; English.
 CC This polypeptide comprises the hepatitis B virus (HBV) 25 kDa (p25)
 CC protein that is encoded by the full-length HBV precore gene.
 CC Evidence is provided that HBV replication is inhibited in the
 CC presence of high levels of HBV precore or precore-related proteins.
 CC These proteins can be incorporated into HBV nucleocapsids along
 CC with the p21 core protein (see W50251), which is the usual
 CC nucleocapsid component, and thereby render the nucleocapsids
 CC deficient in encapsidating HBV pregenomic RNA. Thus, over-
 CC expression of the precore proteins, or certain variants of them,
 CC leads to transdominant inhibition of HBV replication. Suitable
 CC inhibitory proteins include p25, p22 (see W50241), Met-p22 (see
 CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
 CC (see W50238). The inhibitory proteins can be produced by
 CC recombinant methods using claimed expression vectors and host
 CC cells. They can be provided exogenously to the target cells for
 CC use in inhibiting HBV replication. Alternatively, a nucleic acid
 CC construct that directs overexpression of an inhibitory protein in
 CC target cells is used for the gene therapy of HBV infection.
 SQ Sequence 212 AA;

Query Match 60.8%; Score 1375; DB 32; Length 212;
 Best Local Similarity 99.5%; Pred. No. 6.72e-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 gmididykefgatvellsfipstfifsvrldltaasalyrealsepncsphtalrgai 88
 :|||||
 QY 120 SMDIDPYKEGATVELLSFIPSDFFPSVRDLDTASALYREALSEPHCSPHHTALROAI 179

Db 89 lwcgelmrlatwgvnlcdpasrdlvsvyntmglkfifqllwfhlscltfgretvieyl 148
 :|||||
 QY 180 LCGELMTLATWGVNLCDPASRDLVSVYNTMGLKFRQLMFIHISCLTFGRVTIEYL 239
 Db 149 vsfgvwlrtppayrppnapilstlpettvrrrgsprrrrrsgsprrrrrsgsr 208
 :|||||
 QY 240 VSRGVWIRTPPAYRPPNAPILSTLPETTVRRRGSRPRRRTPSPRRRSQSRRRSQSR 299
 Db 209 esgc 212
 :||||
 QY 300 ESQC 303

RESULT 3

ID R27473 standard: Protein; 346 AA.
 AC R27473;
 DT 24-FEB-1993 (first entry)
 DE S12/core protein.
 KM Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
 KM Vaccinia virus; 13L; promoter; NVVAC; recombinant; HBV L;
 KM large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core;
 KM S1; S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;
 KM deletion loci; recipient loci.
 OS Synthetic.
 FH Key
 FT region 1..108
 FT /label S1
 FT region 109..163
 FT /label S2
 FT region 164..346
 FT /label Core
 PN W09215672-A.
 PD 17-SEP-1992.
 PF 09-MAR-1992; U01906.
 PR 07-MAR-1991; US-666056.
 PR 11-JUN-1991; US-713967.
 PR 06-MAR-1992; US-847951.
 PA (VIRO-) VIRGENETICS CORP.
 PI Cox WI, De Talsne C, Francis J, Gettig RR, Johnson GP,
 PI Limpach KJ, Norton EK, Paolletti E, Perkins ME, Plancus SE,
 PI Riviere M, Tartaglia J, Taylor J;
 DR WPI: 92-331718/40.
 DR N-PSDB: Q29105.
 PT Vaccine comprises recombinant, attenuated pox-virus - use for
 PT vaccinating against viral infections such as rabies, hepatitis B,
 PT HIV, HSV, EBV, CMV, mumps etc.
 PS Disclosure: fig 13; 45pp; English.
 CC The sequence given is encoded by an expression cassette which
 CC comprises a portion of the hepatitis B virus (HBV) pre-S region (S12/
 CC core) which is precisely linked to the 1L promoter derived from
 CC vaccinia virus. This DNA sequence was linked to the S1 and S2
 CC sequences and this fragment was used in the construction of a NVVAC
 CC recombinant expressing the HBV gene. Other HBV genes were also used
 CC in the construction. These were HBV M protein (small pre-S antigen,
 CC spsAg) and HBV L (large pre-S antigen, lpsAg). Each of these gene
 CC sequences were inserted individually into three different sites of
 CC NVVAC separated by from each other by large regions of vaccinia DNA
 CC containing essential genes. NVVAC is a Copenhagen vaccine strain of
 CC vaccinia virus which has been modified by deletion of six non-essential
 CC regions of the genome encoding known or potential virulence factors.
 CC The deletion loci were engineered as recipient loci for the insertion
 CC of foreign genes. The spacing of the three inserted sequences ensured
 CC that any recombination that did occur would lead to disruption of the
 CC vaccinia genome and would cause unviable vaccinia virus. See also
 CC Q35501-864.
 SQ Sequence 346 AA;

Query Match 60.8%; Score 1375; DB 5; Length 346;
 Best Local Similarity 99.5%; Pred. No. 6.72e-100;
 Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 163 mdididykefgatvellsfipstfifsvrldltaasalyrealsepncsphtalrgai 222

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QY 120 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALRQAI 179
DB 223 Lcwgelmrlatwgvnledpasrdlvsyvnlnmgkfrqlwfmiscitfgretvleyl 282
QY 180 Lcwgelmrlatwgvnledpasrdlvsyvnlnmgkfrqlwfmiscitfgretvleyl 239
DB 283 vsfgwvltppayrpnpapilstlpetvrrrgsrprtrrpsrrrrsgsrrrrsgsr 342
QY 240 vsfgwvltppayrpnpapilstlpetvrrrgsrprtrrpsrrrrsgsrrrrsgsr 299
DB 343 esgc 346
QY 300 ESQC 303

RESULT 4
ID P80959 standard; protein: 184 AA.
AC P80959;
DT 19-NOV-1990 (first entry)
DE Hepatitis B virus subtype ayw. core protein.
KW Conjugate; fusion protein; hepatitis B core protein; HBV subtype ayw.;
KM T cell stimulating polypeptide; vaccines.
OS Synthetic.
PN EP-271302-A.
PD 15-JUN-1988.
PE 07-DEC-1987; 310725.
PR 07-OCT-1987; US-106538.
PR 07-OCT-1987; US-939617.
PA (SCRIT-) Scripps Clinic Res.
PI Thornton GB, Mortaric AM, Millich DR, McLachlan A.;
DR WPI: 88-153287/24.
PT New conjugates and fusion proteins of immunogenic polypeptide -
PT and hepatitis B core antigen and T cell stimulating polypeptide
PT corep. to core antigen, useful in vaccines.
PS Disclosure; pr. English.
CC This sequence contains the T cell stimulating epitopes, amino acid
CC residue 1-55 and 70-140. It is believed that the regions 1-44 and
CC 70-140 do not contain determinants that suppress T cell activation.
CC Polypeptides essentially consisting of 15 to 55 amino acids
CC corresponding to the above mentioned HBV regions are T cell
CC stimulating. Coupling a polypeptide immunogen to such sequences,
CC e.g. by using a bifunctional reagent which forms a disulphide link,
CC improves its immunogenicity. These are useful in vaccines and can be used
CC therapeutically to improve T cell response to HBcAg in infected
CC subjects.
CC See also P80896-P80898 and P80951-P80959.
SQ Sequence 184 AA;

Query Match 60.2%; Score 1363; DB 1; Length 184;
Best Local Similarity 99.5%; Pred. No. 6,49e-99;
Matches 183; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DT 28-SEP-1998 (first entry)
DE Hepatitis B virus precore p22 polypeptide.
KW Viral replication; inhibitor; HBV; nucleocapsid; gene therapy;
KM Hepatocyte; liver; p22 protein.
OS Hepatitis B virus.
FH Key location/Qualifiers
FT Region 82..98
FT /note= "Immunodominant region"
FN WO9809649-A1.
PD 12-MAR-1998.
PE 03-SEP-1997; U15500.
PR 03-SEP-1996; US-025370.
PA (GEHO) GEN HOSPITAL CORP.
PI Melegari M, Scaglioni PP, Wands JR;
DR WPI: 98-193325/17.
PT DNA encoding proteins which can be incorporated with wild type
PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
PT inhibition of viral replication, especially hepatitis B virus
PS Claim 9; Page 34-35; 60pp; English.
CC This polypeptide comprises the hepatitis B virus (HBV) 22 kDa (p22)
CC protein that is produced by elimination of the 19-amino acid leader
CC peptide from the 25 kDa full-length HBV precore protein (see
CC W50250). Evidence is provided that HBV replication is inhibited in
CC the presence of high levels of HBV precore or precore-related
CC proteins. These proteins can be incorporated into HBV nucleocapsids
CC along with the p21 core protein (see W50251), which is the usual
CC nucleocapsid component, and thereby render the nucleocapsids
CC deficient in encapsidating HBV pregenomic RNA. Thus, over-
CC expression of the precore proteins, or certain variants of them,
CC leads to transdominant inhibition of HBV replication. Suitable
CC inhibitory proteins include p25 (see W50250), p22, Met-p28 (see
CC W50242), p18 (see W50236), Met-p18 (see W50237) and Met-p18-Het
CC (see W50238). Heterologous peptides (see W50244-49) may be
CC inserted into the p22 and Met-p22 polypeptides. The inhibitory
CC proteins can be produced by recombinant methods using claimed
CC expression vectors and host cells. They can be provided exogenously
CC to the target cells for use in inhibiting HBV replication.
CC Alternatively, a nucleic acid construct that directs overexpression
CC of an inhibitory protein in target cells is used for the gene
CC therapy of HBV infection.
SQ Sequence 193 AA;

Query Match 60.1%; Score 1359; DB 3; Length 193;
Best Local Similarity 98.4%; Pred. No. 1.38e-98;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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FT /note= "immunodominant region"
 PN W0909649-A1.
 PD 12-MAR-1998.
 PF 03-SEP-1997: U15500.
 PR 03-SEP-1996: US-025370.
 PA (GEHO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR;
 DR WPI: 98-193325/17.
 PT DNA encoding proteins which can be incorporated with wild type
 PT nucleocapsid subunit(s) into a viral nucleocapsid - useful for
 PT inhibition of viral replication, especially hepatitis B virus
 PS Disclosure: Page 41-42: 60pp: English.
 CC This is the 21 kDa (p21) protein of hepatitis B virus (HBV) that
 CC assembled into a 180 KDa subunit nucleocapsid structure that
 CC promotes viral replication. Evidence is provided that HBV
 CC replication is inhibited in the presence of high levels of HBV
 CC precursor or precursor-related proteins. These proteins can be
 CC incorporated into HBV nucleocapsids along with the p21 core protein
 CC and thereby render the nucleocapsids deficient in encapsidating HBV
 CC pregenomic RNA. Thus, over-expression of the precursor proteins or
 CC certain variants of them, leads to transdominant inhibition of HBV
 CC replication. Suitable inhibitory proteins include p25 (see
 CC W020250), p22 (see W50241), Met-p22 (see W50242), p18 (see W50235),
 CC Met-p18 (see W50237) and Met-p18-Het (see W50238). These proteins
 CC can be produced by recombinant methods using claimed expression
 CC vectors and host cells, and can be provided exogenously to target
 CC cells for use in inhibiting HBV replication. Alternatively, a
 CC nucleic acid construct that directs overexpression of an inhibitory
 CC protein in target cells is used for the gene therapy of HBV
 CC infection.
 SQ Sequence 183 AA;
 Query Match 60.0%; Score 1358; DB 32; Length 183;
 Best Local Similarity 98.9%; Pred. No. 1.67e-98;
 Matches 181; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 mdidpykefgatvellsfipdsffpsvrdlldtasalyrealsepncsphtalrgail 60
 QY 121 MDIDPYKEFGATVELLSFIPDSFFPSVRDLDTASALYREALSEPNCSPHTALRQAIL 180
 Db 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMWHISCLTFRETVELEYLV 120
 QY 181 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMWHISCLTFRETVELEYLV 240
 Db 121 sfgywiltppayrpnapilslipetlvrrrgsprrrtsprrrrsgsrrrrsgsre 180
 QY 241 SFGYWIRTPPAYRPNAPILSLIPETLVRRRGSPRRRTSPRRRRSOSRRRSOSRE 300
 Db 181 sqc 183
 QY 301 SOC 303
 RESULT 7
 ID W09044 Standard: Protein; 183 AA.
 AC W09044;
 DT 11-APR-1997 (first entry)
 DE Hepatitis B virus core protein.
 KM Hepadnavirus: HBV: woodchuck hepatitis virus: hepatitis delta virus;
 KM ground squirrel hepatitis B virus; duck hepatitis B virus;
 KM core protein; replication; antiviral; gene therapy.
 OS Hepatitis B virus.
 FH Key
 FT misc_difference 71..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 71-180 in mutant
 FT polypeptides of the invention (Claim 23)."
 FT misc_difference 81..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 81 and 180 in mutant
 FT polypeptides of the invention (Claim 5)."
 FT misc_difference 171..180
 FT /note= "C-terminus of core protein is at any amino

FT acid position between 171 and 180 in mutant
 FT polypeptides of the invention (Claim 6)."
 FT misc_difference 174..180
 FT /note= "C-terminus of core protein is at any amino
 FT acid position between 174 and 180 in mutant
 FT polypeptides of the invention (Claim 26)."
 FT misc_difference 178
 FT /note= "C-terminus of core protein is at amino acid
 FT position 178 in mutant polypeptides of the
 FT invention (Claim 7)."
 FT misc_difference 178
 FT /note= "C-terminus of core protein is at amino acid
 FT position 178 in mutant polypeptides of the
 FT invention (Claim 7)."
 FT misc_difference 172..183
 FT /note= "amino acid residues 172-183, pref. 174-180,
 FT are deleted from the core protein in mutant
 FT polypeptides of the invention."
 PN W09700698-A1.
 PD 09-JAN-1997.
 PF 20-JUN-1996; U10602.
 PR 20-JUN-1995; US-017814.
 PA (GEHO) GEN HOSPITAL CORP.
 PI Melegari M, Scaglioni PP, Wands JR;
 DR WPI: 97-087176/08.
 DR N-PSDB; T49594.
 PT New method for inhibiting the replication of hepadnaviruses -
 PT comprises introducing a mutant polypeptide with a mutated core
 PT protein or corresponding nucleic acid, for treating, e.g. hepatitis
 PT B.
 PS Claim 5; Page 55-56; 83pp: English.
 CC Alteration of the C-terminus of the core protein (W09044) of
 CC hepatitis B virus (HBV) or other hepadnavirus creates a mutant
 CC polypeptide capable of reducing replication of the wild-type virus
 CC by a dominant negative mechanism. The inhibitory effect is
 CC species-specific and is achieved by deletion of a few C-terminal
 CC amino acids from the core protein, and/or by joining the core
 CC protein to a hepadnavirus surface protein (see also W09045),
 CC creating a core-surface fusion. Such mutant polypeptides (see
 CC also W09046-50) can be used to treat hepadnavirus, e.g. HBV,
 CC infection.
 SQ Sequence 183 AA;
 Query Match 59.8%; Score 1353; DB 20; Length 183;
 Best Local Similarity 98.9%; Pred. No. 4.29e-98;
 Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 1 mdidpykefgatvellsfipdsffpsvrdlldtasalyrealsepncsphtalrgail 60
 QY 121 MDIDPYKEFGATVELLSFIPDSFFPSVRDLDTASALYREALSEPNCSPHTALRQAIL 180
 Db 61 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMWHISCLTFRETVELEYLV 120
 QY 181 CWGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMWHISCLTFRETVELEYLV 240
 Db 121 sfgywiltppayrpnapilslipetlvrrrgsprrrtsprrrrsgsrrrrsgsre 180
 QY 241 SFGYWIRTPPAYRPNAPILSLIPETLVRRRGSPRRRTSPRRRRSOSRRRSOSRE 300
 Db 181 sqc 183
 QY 301 SOC 303
 RESULT 8
 ID R05635 Standard: protein; 183 AA.
 AC R05635;
 DT 30-OCT-1990 (first entry)
 DE Hepatitis B antigen.
 KM Hepatitis B virus; vaccine; HBV; ds.
 OS Synthetic.
 PN RP-374869-A.
 PD 27-JUN-1990.

PF 1-JAN-1989; 123526.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOJ) Biogen Inc.
PI Murray K, Schaller HE;
DR WPI: 90-195067/26.
DR N-PSDB: 004799
PT Recombinant DNA encoding Hepatitis B virus polypeptide antigens -
PS used in detection of infection and in vaccine prodn.
PS Disclosure: 4pp; English.
CC Polypeptide fragments encoded by the DNA sequence are antigenic for
CC HBV and may be used as a vaccine or in detection. Peptides may be
CC cultured in a suitable bacterial host such as E.coli.
CC Fragments of the sequence are also claimed as being antigenically
CC useful.
SQ Sequence 183 AA;

Query Match 59.6%; Score 1349; DB 1; Length 183;
Best Local Similarity 96.7%; Pred. No. 9.14e-98;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdipkyefgatlvelsfpsdffpsrvdlldtaalyrdalesepshphltargail 60
|||||
QY 121 MDIPKKEFGATVELLSFLPSDFPSPRDLDLTASALYREALSEPHCSPHHTLRQAAIL 180
Db 61 cwgdlmclatwgvnledpsardlvsvyvtntnglkfgrllwfhscitfgrevleylv 120
|||||
QY 181 CWGELMTLATWGVNLEDPSARDLVSVYVTNTNGLKFQRLMHISCLTFRREVIVELYV 240
Db 121 sfgywiltppayrpnapilslipetvrrrgsprrrpsrrrrsgsrrrrsgsrr 180
|||||
QY 241 SFGWIRTPPAYRPPNAPILSLIPETVRRRGSPRRRTPSPRRRSQSPRRRSQSRRE 300
Db 181 sqc 183
|||
QY 301 SQC 303

RESULT 9

ID P00041 standard; Protein; 183 AA.
AC P00041;
DT 14-OCT-1992 (first entry)
DE Sequence of core antigen.
KM Hepatitis B virus; antigen: antibody; diagnosis; vaccine.
OS Hepatitis B virus.
PS EP-13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979; 303017.
PR 22-DEC-1978; GB-049907.
PR 27-DEC-1978; GB-050039.
PR 01-NOV-1979; GB-037910.
PA (BIOJ) Biogen Inc.
PI Murray K, Schaller HE;
DR WPI: 80-57268C/33.
DR N-PSDB: N00003.
PT Recombinant DNA coding for polypeptide - have specificity of
PT hepatitis B viral antigens in detection or antibody stimulation
PS Example: Figs 3-4; 43pp; English.
CC Human serum from a single HBsAg positive, HBeAg positive donor
CC (serotype adym) was used to prep. a DNA-contg. pellet which was
CC labelled with 3H or 32P as described by P. M. Kaplan et al (1973).
CC The labelled DNA was then extracted with phenol from the resulting
CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
CC It was then cloned in plasmid pBR322 which was used to transform E.
CC coli. Micro-organisms prep. by the processes are deposited at the
CC NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dg;
CC HBV-Xpn I dg; Tetr Amps HBV+.
SQ Sequence 183 AA;

Query Match 59.6%; Score 1349; DB 5; Length 183;
Best Local Similarity 96.7%; Pred. No. 9.14e-98;
Matches 177; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 mdipkyefgatlvelsfpsdffpsrvdlldtaalyrdalesepshphltargail 60
|||||
QY 121 MDIPKKEFGATVELLSFLPSDFPSPRDLDLTASALYREALSEPHCSPHHTLRQAAIL 180
Db 61 cwgdlmclatwgvnledpsardlvsvyvtntnglkfgrllwfhscitfgrevleylv 120
|||||
QY 181 CWGELMTLATWGVNLEDPSARDLVSVYVTNTNGLKFQRLMHISCLTFRREVIVELYV 240
Db 121 sfgywiltppayrpnapilslipetvrrrgsprrrpsrrrrsgsrrrrsgsrr 180
|||||
QY 241 SFGWIRTPPAYRPPNAPILSLIPETVRRRGSPRRRTPSPRRRSQSPRRRSQSRRE 300
Db 181 sqc 183
|||
QY 301 SQC 303

Query Match 59.4%; Score 1344; DB 20; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.35e-97;
Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mdipkyefgatlvelsfpsdffpsrvdlldtaalyrdalesepshphltargail 60
|||||
QY 121 MDIPKKEFGATVELLSFLPSDFPSPRDLDLTASALYREALSEPHCSPHHTLRQAAIL 180
Db 61 cwgdlmclatwgvnledpsardlvsvyvtntnglkfgrllwfhscitfgrevleylv 120
|||||
QY 181 CWGELMTLATWGVNLEDPSARDLVSVYVTNTNGLKFQRLMHISCLTFRREVIVELYV 240
Db 121 sfgywiltppayrpnapilslipetvrrrgsprrrpsrrrrsgsrrrrsgsrr 179
|||||

Query 241 SEGVWIRTPPAYRPPNAPILSTLPETTVVARRGRSPRRRTSPRRRSOSPRRRRSOSR 299

RESULT 11
ID P00004 standard; Protein: 184 AA.
AC P00004;
DT 14-OCT-1992 (first entry)
DE Sequence of core antigen.
KW Hepatitis B virus; antigen; antibody; diagnosis; vaccine.
OS Hepatitis B virus.
PN EP--13828-A.
PD 06-AUG-1980.
PF 21-DEC-1979: 303017.
PR 22-DEC-1978: GB-049907.
PR 27-DEC-1978: GB-050039.
PR 01-NOV-1979: GB-037910.
PA (BIOT) BIOGEN NV.
PI Murray K, Schaller HE.
DR WPI: 80-57268C/33.
DR N-PSDB; N00002.
PT Recombinant DNA coding for polypeptide - have specificity of
PS Hepatitis B viral antigens in detection or antibody stimulation
PS Clam 13; Page 40; 43pp; English.
CC (serotype adym) was used to prep. a DNA-contg. pellet which was
CC Human serum from a single HBSAg positive, HBeAg positive donor
CC labeled with 3H or 32P as described by P. M. Kaplan et al (1973).
CC The labeled DNA was then extracted with phenol from the resulting
CC pellet using the procedure of L. I. Lutwick and W. S. Robinson (1977).
CC It was then cloned in plasmid pBR322 which was used to transform E.
CC coli. Micro-organisms prep. by the processes are deposited at the
CC NCIB as pBR322-HBV-G-L, e.g. E. coli HB101/pBR322-Pst I dg:
CC HBV-kpn I dc: Tetr Amps HBV+.
SQ Sequence 184 AA:

Query Match 59.1%; Score 1338; DB 5; Length 184;
Best Local Similarity 96.2%; Pred. No. 7.30e-97;
Matches 177; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

DB 1 mdidpykefagavellslfspdffpsvrcdlldtaaalrydalespeshcphtalrgai 60
OY 121 MDIDPYKEGATVELLSFLPSDFPSV-RDLDTASALYREALSPESHCPHTALRQAI 179
DB 61 lcwgdmlatwvgnldpasrdlvsyvnmnglkfrqlwfhiscldtfgretvleyl 120
OY 180 LCWGEMLTATWGVNLEDPASRDLVSYVNTMNGLKFRQLWFHISCLTFGRETVLEYL 239
DB 121 vsfgwvrtppayrppnapilslpettvrrrgisprrrpsrrrrsqsprrrrsqr 180
OY 240 VSEGVWIRTPPAYRPPNAPILSTLPETTVVARRGRSPRRRTSPRRRSOSPRRRRSOSR 299
DB 181 esgc 184 /
OY 300 ESGC 303
RESULT 12
ID R40808 standard; Protein: 208 AA.
AC R40808;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 / IL-1 Fusion.
KW Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Synthetic.
FH Key Location/Qualifiers
FT region 8..19 /label= PV-1
FT region 20..25 /label= IL-1
FT protein 26..208 /label= HBC
FT J05192170-A.
PN 03-AUG-1993.
PF 24-SEP-1991: 243800.

PR 24-SEP-1991: JP-243800.
PA (NISW) NISSHIN OIL MILLS LTD.
DR WPI: 93-277479/35.
DR N-PSDB: 047738.
PT Recombinant plasmid for high immunogenicity virus - contains
PT recombinant haemagglutinin gene, hepatitis B core gene of vaccinia
PT virus and exotic genes
PS Disclosure; Fig 9; 12pp; Japanese.
CC The hepatitis B core gene is recombinant with PV-1 DNA
CC and IL-1 beta to form a plasmid (047738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.
SQ Sequence 208 AA:

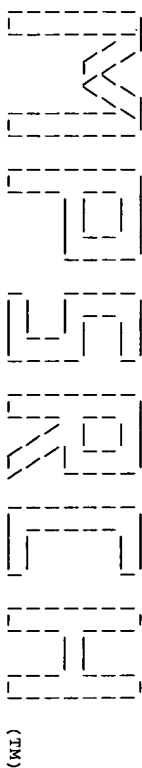
Query Match 59.1%; Score 1337; DB 8; Length 208;
Best Local Similarity 94.6%; Pred. No. 8.82e-97;
Matches 175; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

DB 24 lsmdidpykefagavellslfspdffpsvrcdlldtaaalrydalespeshcphtalrgai 83
OY 119 LSMDIDPYKEGATVELLSFLPSDFPSV-RDLDTASALYREALSPESHCPHTALRQAI 178
DB 84 lcwgdmlatwvgnldpasrdlvsyvnmnglkfrqlwfhiscldtfgretvleyl 143
OY 179 LCWGEMLTATWGVNLEDPASRDLVSYVNTMNGLKFRQLWFHISCLTFGRETVLEY 238
DB 144 lvsfgwvrtppayrppnapilslpettvrrrgisprrrpsrrrrsqsprrrrsqr 203
OY 239 LVSEGVWIRTPPAYRPPNAPILSTLPETTVVARRGRSPRRRTSPRRRSOSPRRRRSOS 298
DB 204 resgc 208
OY 299 RESGC 303

RESULT 13
ID R40806 standard; Protein: 196 AA.
AC R40806;
DT 16-FEB-1994 (first entry)
DE Hepatitis B core / PV-1 fusion.
KW Hepatitis B; core; HBC; PV-1; IL-1 beta; interleukin; plasmid.
OS Synthetic.
FH Key Location/Qualifiers
FT region 7..13 /label= PV-1
FT protein 14..196 /label= HBC
PN J05192170-A.
PD 03-AUG-1993.
PF 24-SEP-1991: 243800.
PR (NISW) NISSHIN OIL MILLS LTD.
PA WPI: 93-277479/35.
DR N-PSDB: 047736.
PT Recombinant plasmid for high immunogenicity virus - contains
PT recombinant haemagglutinin gene, hepatitis B core gene of vaccinia
PT virus and exotic genes
PS Disclosure; Fig 7; 12pp; Japanese.
CC The hepatitis B core gene is recombinant with PV-1 DNA
CC and IL-1 beta to form a plasmid (047738) which is then used to produce
CC a vaccine. NB: Sequence is difficult to read in the original
CC specification.
SQ Sequence 196 AA:

Query Match 59.0%; Score 1336; DB 8; Length 196;
Best Local Similarity 95.1%; Pred. No. 1.07e-96;
Matches 175; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

DB 13 amdidpykefagavellslfspdffpsvrcdlldtaaalrydalespeshcphtalrgai 72
OY 120 AMDIDPYKEGATVELLSFLPSDFPSV-RDLDTASALYREALSPESHCPHTALRQAI 179
DB 73 lcwgdmlatwvgnldpasrdlvsyvnmnglkfrqlwfhiscldtfgretvleyl 132



(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Dec 16 13:35:44 1999; Maspar time 14.81 Seconds
Tabular output not generated. 820.017 Million cell updates/sec

Title: >US3890-1-38183
Description: (1-303) from us3890-1-38183.pep
Perfect Score: 2263
Sequence: 1 MDIDYKEGATVELLSFLP.....RRRRSQSPRRRRSQSRNSQC 303

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr60
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 47.447; Variance 117.780; scale 0.403

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1375	60.8	212	1	NKVLAH e antigen precursor / 1.94e-202	
2	1373	60.7	183	2	S53207 core antigen - hepati / 4.22e-202	
3	1374	60.7	212	2	S53211 e antigen precursor / 2.66e-202	
4	1374	60.7	212	2	S53204 e antigen precursor / 2.66e-202	
5	1373	60.7	212	2	S20750 e antigen precursor / 4.22e-202	
6	1370	60.5	183	2	S53270 core antigen - hepati / 1.36e-201	
7	1370	60.5	212	2	S53216 e antigen precursor / 1.36e-201	
8	1370	60.5	212	2	S53272 e antigen precursor / 1.36e-201	
9	1369	60.5	212	2	S53163 e antigen precursor / 2.01e-201	
10	1369	60.5	212	2	S20746 e antigen precursor / 2.01e-201	
11	1369	60.5	212	2	S53225 e antigen precursor / 2.01e-201	
12	1368	60.5	212	2	S53198 e antigen precursor / 2.96e-201	
13	1366	60.4	212	2	S53223 e antigen precursor / 6.45e-201	
14	1366	60.4	212	2	S53274 e antigen precursor / 6.45e-201	
15	1364	60.3	183	2	S53169 core antigen - hepati / 1.41e-200	
16	1363	60.2	183	2	S53247 core antigen - hepati / 2.08e-200	
17	1363	60.2	212	2	S53202 e antigen precursor / 2.08e-200	
18	1363	60.2	212	2	S53159 e antigen precursor / 2.08e-200	
19	1363	60.2	212	2	S53200 e antigen precursor / 3.07e-200	
20	1362	60.2	212	2	S53251 e antigen precursor / 6.68e-200	
21	1360	60.1	212	2	S53204 e antigen precursor / 6.68e-200	
22	1360	60.1	212	2	S53227 e antigen precursor / 9.87e-200	
23	1359	60.1	212	2	S53253 e antigen precursor / 9.87e-200	

24	1358	60.0	211	1	NKVLAI e antigen precursor / 1.46e-199
25	1357	60.0	212	2	S53281 e antigen precursor / 2.15e-199
26	1355	59.9	212	1	NKVLBH e antigen precursor / 4.69e-199
27	1355	59.9	212	2	S53242 e antigen precursor / 4.69e-199
28	1351	59.7	183	2	S53129 core antigen - hepati / 2.23e-198
29	1351	59.7	212	2	S53240 core antigen - hepati / 2.23e-198
30	1349	59.6	183	1	NKVLAI core antigen - hepati / 4.85e-198
31	1349	59.6	183	2	S53181 core antigen - hepati / 4.85e-198
32	1348	59.6	183	2	S53232 core antigen - hepati / 7.16e-198
33	1348	59.6	183	2	S53260 core antigen - hepati / 7.16e-198
34	1345	59.4	183	2	S53152 core antigen - hepati / 2.30e-197
35	1344	59.4	212	2	S53229 e antigen precursor / 3.40e-197
36	1343	59.3	183	2	S53214 core antigen - hepati / 5.02e-197
37	1342	59.3	183	2	S53140 core antigen - hepati / 7.40e-197
38	1341	59.3	183	2	S53267 core antigen - hepati / 1.09e-196
39	1341	59.3	183	2	S53189 core antigen - hepati / 1.09e-196
40	1341	59.3	212	2	S53238 e antigen precursor / 1.09e-196
41	1339	59.2	183	2	S53137 core antigen - hepati / 2.38e-196
42	1340	59.2	212	2	S53257 e antigen precursor / 1.61e-196
43	1339	59.2	212	2	S52651 e antigen precursor / 2.38e-196
44	1338	59.1	212	2	S53236 e antigen precursor / 3.51e-196
45	1337	59.1	212	1	NKVLJ2 e antigen precursor / 5.19e-196

ALIGNMENTS

RESULT 1
ENTRY NKVLAH #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw4, isolate hb321 and others)
ALTERNATE_NAMES HBE antigen precursor / HBC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal name hepatitis B virus; HBV
#subtype ayw4, isolate hb321; isolate patient Ferracuti '83;
isolate patient Castag '85; isolate patient Sanna '84;
isolate patient Licheri '1'85; isolate patient Flore '1'86;
isolate patient Licheri '83
18-Dec-1981 #sequence_revision 08-Nov-1996 #text_change
10-Oct-1997
DATE
ACCESSIONS S47405; S53191; S53209; S53234; S53264; S53249; S53262;
S53277; A03711
REFERENCE S47404
#authors Plucieniczak, A.
#submission Submitted to the EMBL Data Library, August 1994
#description Molecular cloning and sequencing of two complete genomes of
polish isolates of human hepatitis B virus.
#accession S47405
#molecule_type DNA
#residues 1-212 #label PLU
#cross-references EMBL:235716; NID:9527435; PID:9527437
##experimental_source subtype ayw4, isolate hb321
REFERENCE S53112
#authors Lai, M.E.; Marzoleri, A.P.; Porru, A.; Balestrieri, A.
#submission Submitted to the EMBL Data Library, March 1995
#accession S53191
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X85283; NID:g736088; PID:g736090
##experimental_source Isolate patient Ferracuti '83
#accession S53209
#molecule_type DNA
#residues 1-212 #label LA2
#cross-references EMBL:X85290; NID:g736114; PID:g736116
##experimental_source Isolate patient Castag '83
#accession S53234
#molecule_type DNA
#residues 1-212 #label LA3
#cross-references EMBL:X85300; NID:g736150; PID:g736152
##experimental_source Isolate patient Sanna '84
#accession S53264
#molecule_type DNA
#residues 1-212 #label LA4
#cross-references EMBL:X85313; NID:g736194; PID:g736196

##experimental_source isolate patient Licheri-1'85
#accession S53249
##molecule_type DNA
##residues 1-212 ##label LA5
##cross-references EMBL:X85306; NID:g736172; PID:g736174
##experimental_source isolate patient Fiore-1'86
#accession S53262
##molecule_type DNA
##residues 1-212 ##label LA6
##cross-references EMBL:X85312; NID:g736191; PID:g736193
##experimental_source isolate patient Licheri'83
#accession S53277
##molecule_type DNA
##residues 30-212 ##label LA7
##cross-references EMBL:X85317; NID:g736211; PID:g736214
##experimental_source patient Giordo-2'86
##note due to a stop codon between the alternative initiators
the e antigen precursor cannot be processed

REFERENCE
#authors A93214
Galibert, F.; Mandart, E.; Fltoussi, F.; Tlollais, P.;
Charney, P.
#journal Nature (1979) 281:646-650
#title Nucleotide sequence of the hepatitis B virus genome (subtype
ayw) in E. coli.
#cross-references M01D:81012091
#accession A03711
##molecule_type DNA
##residues 1-212 ##label GAL
##cross-references GB:J02203; NID:g329640; PID:g329642
##experimental_source subtype ayw

GENETICS
#gene C
#CLASSIFICATION #superfamily hepatitis B virus core antigen
#KEYWORDS alternative initiators; core protein

FEATURE
1-29
30-212 #domain signal sequence #status predicted #label SIG\
30-178 #product core antigen #status predicted #label CAG\
179-212 #domain carboxyl-terminal propeptide #link EAG #status
predicted #label ECP

SUMMARY
#length 212 #molecular-weight 24350 #checksum 782

Query Match 60.8%; Score 1375; DB 1; Length 212;
Best Local Similarity 99.5%; Pred. No. 1.94e-202;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKRGATVELSLFSPDFPSVRDLDTASALYRDALSPHCSPHHTALRQAI 88
:|||||
QY 120 SMIDPKRGATVELSLFSPDFPSVRDLDTASALYRDALSPHCSPHHTALRQAI 179
:|||||
Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGLEFRQLMFHISCLTFGRVIEYL 148
:|||||
QY 180 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGLEFRQLMFHISCLTFGRVIEYL 239
:|||||
Db 149 VSGVWIRTPPAIRPPAPILSTIPETTVYRRGRSPRRRTPSRRRSOSPRRRRSOSR 208
:|||||
QY 240 VSGVWIRTPPAIRPPAPILSTIPETTVYRRGRSPRRRTPSRRRSOSPRRRRSOSR 299
:|||||
Db 209 ESOC 212
:|||||
QY 300 ESOC 303

RESULT 2
ENTRY S53207 #type complete
TITLE core antigen - hepatitis B virus (isolate patient
Castaa-2'87)

ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Castaa-2'87
#variety 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53207
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53207
##molecule_type DNA
##residues 1-183 ##label LA1
##cross-references EMBL:X85289; NID:g736110; PID:g736113
##experimental_source isolate patient Castaa-2'87
##note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
#CLASSIFICATION #superfamily hepatitis B virus core antigen
#KEYWORDS core protein
#SUMMARY #length 183 #molecular-weight 21102 #checksum 2165

Query Match 60.7%; Score 1373; DB 2; Length 183;
Best Local Similarity 99.5%; Pred. No. 4.22e-202;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MDIDPKRGATVELSLFSPDFPSVRDLDTASALYRDALSPHCSPHHTALRQAI 60
:|||||
QY 121 MDIDPKRGATVELSLFSPDFPSVRDLDTASALYRDALSPHCSPHHTALRQAI 180
:|||||
Db 61 CMGELMTLATWGVNLEDPASRDVSVYNTNMGLEFRQLMFHISCLTFGRVIEYL 120
:|||||
QY 181 CMGELMTLATWGVNLEDPASRDVSVYNTNMGLEFRQLMFHISCLTFGRVIEYL 240
:|||||
Db 121 SFGVWIRTPPAIRPPAPILSTIPETTVYRRGRSPRRRTPSRRRSOSPRRRRSOSR 180
:|||||
QY 241 SFGVWIRTPPAIRPPAPILSTIPETTVYRRGRSPRRRTPSRRRSOSPRRRRSOSR 300
:|||||
Db 181 SOC 183
:|||||
QY 301 SOC 303

RESULT 3
ENTRY S53211 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(isolate patient Castag-1'85 and others)

ALTERNATE_NAMES HBC antigen; HBe antigen precursor / HBC antigen; pre-C/C
antigen

CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus, HBV
#variety isolate patient Castag-1'85; isolate patient Ferracuti-1'89
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
08-Sep-1997

ACCESSIONS S53211; S53197
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission submitted to the EMBL Data Library, March 1995
#accession S53211
##molecule_type DNA
##residues 1-212 ##label LA1
##cross-references EMBL:X85291; NID:g736117; PID:g736119
##experimental_source isolate patient Castag-1'85
#accession S53197
##molecule_type DNA
##residues 30-212 ##label LAW
##cross-references EMBL:X85284; NID:g736095; PID:g736098
##experimental_source isolate patient Ferracuti-1'89
##note due to a stop codon between the alternative initiators
the e antigen precursor cannot be produced

GENETICS
#gene C
#CLASSIFICATION #superfamily hepatitis B virus core antigen
#KEYWORDS alternative initiators; core protein
#FEATURE
1-29
30-212 #domain signal sequence #status predicted #label SIG\
#product core antigen #status predicted #label CAG\
#product e antigen #status predicted #label EAG\
30-178

179-212 #domain carboxyl-terminal propeptide #link EAG #status
#predicted #label ECP
SUMMARY #length 212 #molecular-weight 24336 #checksum 746

Query Match
Best Local Similarity 98.9%; Pred. No. 2,866-202;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAI 88
Qy 120 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAI 179

Db 89 LCMGDLMTLATWGVNLEDPAASRDLYSVYNTNGLKFRQLMWHISCLTGTGRETVIEL 148
Qy 180 LCMGELMTLATWGVNLEDPAASRDLYSVYNTNGLKFRQLMWHISCLTGTGRETVIEL 239

Db 149 VSEFWMTPTAPPYPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 208
Qy 240 VSEFWMTPTAPPYPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 299

Db 209 ESQC 212
Qy 300 ESQC 303

RESULT 4
ENTRY S32204 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C1000)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus; HBV
#subtype ayw, patient C1000
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS
REFERENCE S32202
PRESTIER-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Gerok, W.; Rasenack, J.
#submission submitted to the EMBL Data Library, March 1993
#description Identification and sequence analysis of hepatitis B virus DNA in immunological negative infection.
#accession S32204
#molecule_type DNA
#residues 1-212 #label PRE
#cross-references EMBL:X72702; NID:q288927; PID:q288930
#experimental_source subtype ayw, patient C1000
#note due to a stop codon between the alternative initiators the e antigen precursor cannot be produced

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS core protein
FEATURE 1-29
1-29
30-212 #domain signal sequence #status predicted #label SIG
30-178 #product core antigen #status predicted #label CAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24336 #checksum 770

Query Match
Best Local Similarity 98.9%; Pred. No. 2,866-202;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAI 88
Qy 120 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAI 179

Db 89 LCMGDLMTLATWGVNLEDPAASRDLYSVYNTNGLKFRQLMWHISCLTGTGRETVIEL 148
Qy 180 LCMGELMTLATWGVNLEDPAASRDLYSVYNTNGLKFRQLMWHISCLTGTGRETVIEL 239

Db 149 VSEFWMTPTAPPYPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 208
Qy 240 VSEFWMTPTAPPYPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 299

Db 209 ESQC 212
Qy 300 ESQC 303

RESULT 5
ENTRY S20750 #type complete
TITLE e antigen precursor / core antigen - hepatitis B virus
(subtype ayw, patient C1)
ALTERNATE_NAMES HBe antigen precursor / HBeC antigen; pre-C/C antigen
CONTAINS core antigen; e antigen
ORGANISM #formal_name hepatitis B virus; HBV
#subtype ayw, patient C1
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS
REFERENCE S20750
PRESTIER-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Gerok, W.; Rasenack, J.
#submission submitted to the EMBL Data Library, March 1992
#description Sequence analysis of HBV genomes isolated from patients with HBsAg negative chronic liver disease.
#accession S20750
#molecule_type DNA
#residues 1-212 #label LAI
#cross-references EMBL:X65258; NID:q59434; PID:q59436
#experimental_source subtype ayw, patient C1

GENETICS
#gene C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS alternative initiators; core protein
FEATURE 1-29
30-212 #domain signal sequence #status predicted #label SIG
30-178 #product core antigen #status predicted #label CAG
179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 147

Query Match
Best Local Similarity 98.9%; Pred. No. 4,226-202;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAI 88
Qy 120 SMDIDPKKEGATVELLSFLPSDFPSVRLDLDTSALYREALSPHCSPHHTALRQAI 179

Db 89 LCMGDLMTLATWGVNLEDPAASRDLYSVYNTNGLKFRQLMWHISCLTGTGRETVIEL 148
Qy 180 LCMGELMTLATWGVNLEDPAASRDLYSVYNTNGLKFRQLMWHISCLTGTGRETVIEL 239

Db 149 VSEFWMTPTAPPYPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 208
Qy 240 VSEFWMTPTAPPYPPNAPILSTLPETTVARRGRSPRRRTPSPRRRSQSPRRRSQSR 299

Db 209 ESQC 212
Qy 300 ESQC 303

RESULT 6
ENTRY S53270 #type complete
TITLE e antigen - hepatitis B virus (isolate patient Licheri-2/87)
ALTERNATE_NAMES HBeC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus; HBV
#isolate patient Licheri-2/87
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change

DB	29	GMDIDPYKEFGATVLLSFLPSDFPSRDLIDNASALYREALSEPCSPHHTALRAI	88
QY	120	SMDIDPYKEFGATVLLSFLPSDFPSRDLIDNASALYREALSEPCSPHHTALRAI	179
Db	89	LCWGLMLTLATWGVNLDPSRDLVSVYVNTNMGLKFRQLMFIISCLTGFRETIVELYL	148
QY	180	LCWGLMLTLATWGVNLDPSRDLVSVYVNTNMGLKFRQLMFIISCLTGFRETIVELYL	239
Db	149	VSFQWITTPAPYRPNPAPILSTLPEITVVRGRGSPRRRTPPSPRRRSQSPRRRSQSR	208
QY	240	VSFQWITTPAPYRPNPAPILSTLPEITVVRGRGSPRRRTPPSPRRRSQSPRRRSQSR	299
Db	209	ESQC 212	
QY	300	ESQC 303	
RESULT	8		
ENTRY	553272	#type complete	
TITLE	e antigen precursor / core antigen - hepatitis B virus (isolate patient Licheri-3'90)		
ALTERNATE_NAMES	HBe antigen precursor / HBeC antigen; pre-C/C antigen		
CONTAINS	core antigen; e antigen		
ORGANISM	#formal_name hepatitis B virus, HBV		
DATE	#isolate patient Licheri-3'90 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997		
ACCESSIONS	553272		
REFERENCE	553112		
#authors	Lai, M.E.; Mazzeoli, A.P.; Porru, A.; Balestrieri, A.		
#submission	submitted to the EMBL Data Library, March 1995		
#accession	553272		
#molecule_type	DNA		
#residues	1-212	#label LAI	
#cross_references	EMBL:X85315; NID:g736205; PID:g736207		
#experimental_source	isolate patient Licheri-3'90		
GENETICS			
#gene	C		
CLASSIFICATION	#superfamily hepatitis B virus core antigen		
KEYWORDS	alternative initiators; core protein		
FEATURE			
1-29	#domain signal sequence #status predicted #label SIG\		
30-212	#product core antigen #status predicted #label CAG\		
30-178	#product e antigen #status predicted #label EAG\		
179-212	#domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP		
SUMMARY	#length 212	#molecular_weight 24366	#checksum 446
Query Match	60.5%;	Score 1370;	DB 2; Length 212;
Best Local Similarity	98.9%;	Pred. No. 1.36e-201;	
Matches 182;	Conservative 1;	Mismatches 1;	Indels 0; Gaps 0
Db	29	GMDIDPYKEFGATVLLSFLPSDFPSRDLIDNASALYREALSEPCSPHHTALRAI	88
QY	120	SMDIDPYKEFGATVLLSFLPSDFPSRDLIDNASALYREALSEPCSPHHTALRAI	179
Db	89	LCWGLMLTLATWGVNLDPSRDLVSVYVNTNMGLKFRQLMFIISCLTGFRETIVELYL	148
QY	180	LCWGLMLTLATWGVNLDPSRDLVSVYVNTNMGLKFRQLMFIISCLTGFRETIVELYL	239
Db	149	VSFQWITTPAPYRPNPAPILSTLPEITVVRGRGSPRRRTPPSPRRRSQSPRRRSQSR	208
QY	240	VSFQWITTPAPYRPNPAPILSTLPEITVVRGRGSPRRRTPPSPRRRSQSPRRRSQSR	299
Db	209	ESQC 212	
QY	300	ESQC 303	
RESULT	9		
ENTRY	553163	#type complete	
TITLE	e antigen precursor / core antigen - hepatitis B virus		

ALTERNATE_NAMES (isolate patient Vitorina'92)
 CONTRAINS HBe antigen precursor / HBeC antigen: pre-C/C antigen
 ORGANISM core antigen; e antigen
 #formal_name hepatitis B virus, HBV
 #variety isolate patient Vitorina'92
 DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53163
 REFERENCE S53112
 #authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 #submission submitted to the EMBL Data Library, March 1995
 #accession S53163
 #molecule_type DNA
 #residues 1-212 #label LAI
 #cross-references EMBL:X85256; NID:g736050; PID:g736052
 ##experimental_source isolate patient Vitorina'92

GENETICS C
 #gene #superfamily hepatitis B virus core antigen
 #key_words alternative initiators; core protein
 FEATURE
 1-29 #domain signal sequence #status predicted #label SIG\
 30-212 #product core antigen #status predicted #label CAG\
 30-178 #product e antigen #status predicted #label EAG\
 179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24322 #checksum 842

Query Match 60.5%; Score 1369; DB 2; Length 212;
 Best Local Similarity 98.9%; Pred. No. 2,01e-201;
 Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
 :|||||
 Qy 120 SMDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 179
 :|||||

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQRLMFHISCLTFCGRTVIEYL 148
 :|||||
 Qy 180 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQRLMFHISCLTFCGRTVIEYL 239
 :|||||

Db 149 VSGFWIRTPPAYRPPNAPILSTLPETTVRRRGRSPRRRTSPRRRSQSPRRRSOSR 208
 :|||||
 Qy 240 VSGFWIRTPPAYRPPNAPILSTLPETTVRRRGRSPRRRTSPRRRSQSPRRRSOSR 299
 :|||||

Db 209 ESQC 212
 :|||||
 Qy 300 ESQC 303

RESULT 10
 ENTRY S20746 #type complete
 TITLE e antigen precursor / core antigen - hepatitis B virus
 (subtype ayw, patient C)
 ALTERNATE_NAMES HBe antigen precursor / HBeC antigen: pre-C/C antigen
 CONTRAINS core antigen; e antigen
 ORGANISM #formal_name hepatitis B virus, HBV
 #variety subtype ayw, patient C
 DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

ACCESSIONS S20746
 REFERENCE S20745
 #authors Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
 #submission submitted to the EMBL Data Library, March 1992
 #description Sequence analysis of HBV genomes isolated from patients with HBsAg negative chronic liver disease.

#accession S20746
 #molecule_type DNA
 #residues 1-212 #label LAI
 #cross-references EMBL:X65257; NID:g59429; PID:g59431
 ##experimental_source subtype ayw, patient C

GENETICS C
 #gene

CLASSIFICATION #superfamily hepatitis B virus core antigen
 KEYWORDS alternative initiators; core protein
 FEATURE
 1-29 #domain signal sequence #status predicted #label SIG\
 30-212 #product core antigen #status predicted #label CAG\
 30-178 #product e antigen #status predicted #label EAG\
 179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24348 #checksum 506

Query Match 60.5%; Score 1369; DB 2; Length 212;
 Best Local Similarity 98.4%; Pred. No. 2,01e-201;
 Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
 :|||||
 Qy 120 SMDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 179
 :|||||

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQRLMFHISCLTFCGRTVIEYL 148
 :|||||
 Qy 180 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQRLMFHISCLTFCGRTVIEYL 239
 :|||||

Db 149 VSGFWIRTPPAYRPPNAPILSTLPETTVRRRGRSPRRRTSPRRRSQSPRRRSOSR 208
 :|||||
 Qy 240 VSGFWIRTPPAYRPPNAPILSTLPETTVRRRGRSPRRRTSPRRRSQSPRRRSOSR 299
 :|||||

Db 209 ESQC 212
 :|||||
 Qy 300 ESQC 303

RESULT 11
 ENTRY S53225 #type complete
 TITLE e antigen precursor / core antigen - hepatitis B virus
 (isolate patient Chigline-2'86)
 ALTERNATE_NAMES HBe antigen precursor / HBeC antigen: pre-C/C antigen
 CONTRAINS core antigen; e antigen
 ORGANISM #formal_name hepatitis B virus, HBV
 #variety isolate patient Chigline-2'86
 DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Sep-1997

ACCESSIONS S53225
 REFERENCE S53112
 #authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 #submission submitted to the EMBL Data Library, March 1995
 #accession S53225
 #molecule_type DNA
 #residues 1-212 #label LAI
 #cross-references EMBL:X85256; NID:g736137; PID:g736139
 ##experimental_source isolate patient Chigline-2'86

GENETICS C
 #gene #superfamily hepatitis B virus core antigen
 #key_words alternative initiators; core protein
 FEATURE
 1-29 #domain signal sequence #status predicted #label SIG\
 30-212 #product core antigen #status predicted #label CAG\
 30-178 #product e antigen #status predicted #label EAG\
 179-212 #domain carboxyl-terminal propeptide #link EAG #status predicted #label ECP

SUMMARY #length 212 #molecular-weight 24308 #checksum 655

Query Match 60.5%; Score 1369; DB 2; Length 212;
 Best Local Similarity 98.4%; Pred. No. 2,01e-201;
 Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88
 :|||||
 Qy 120 SMDIPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 179
 :|||||

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQRLMFHISCLTFCGRTVIEYL 148
 :|||||
 Qy 180 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKRFQRLMFHISCLTFCGRTVIEYL 239
 :|||||

Qy	Dy	ESOC	ESOC
149	209	212	208
VSFGWITTPATYRPPNAPILSTLPETTVARRGRSPRRRTPSRRRSOSPRRRRSQR	VSFGWITTPATYRPPNAPILSTLPETTVARRGRSPRRRTPSRRRSOSPRRRRSQR	VSFGWITTPATYRPPNAPILSTLPETTVARRGRSPRRRTPSRRRSOSPRRRRSQR	VSFGWITTPATYRPPNAPILSTLPETTVARRGRSPRRRTPSRRRSOSPRRRRSQR
240	300	303	299
VSFGWITTPATYRPPNAPILSTLPETTVARRGRSPRRRTPSRRRSOSPRRRRSQR	VSFGWITTPATYRPPNAPILSTLPETTVARRGRSPRRRTPSRRRSOSPRRRRSQR	VSFGWITTPATYRPPNAPILSTLPETTVARRGRSPRRRTPSRRRSOSPRRRRSQR	VSFGWITTPATYRPPNAPILSTLPETTVARRGRSPRRRTPSRRRSOSPRRRRSQR

RESULT	12	
ENTRY		
TITLE	S53198	#type complete
	e antigen precursor / core antigen -	hepatitis B virus
	(isolate patient Ferracuti-2'90)	
ALTERNATE_NAMES	HBe antigen precursor / HBe antigen;	pre-C/C antigen
CONTAINS	core antigen; e antigen	
ORGANISM	#formal_name hepatitis B virus, HBV	
#variety	isolate patient Ferracuti-2'90	
DATE	08-Jul-1995	#sequence_revision 03-Aug-1995
	08-Sep-1997	#text_change

```

ACCESSIONS      553198
REFERENCE        553112
#authors         Lai, M.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submission      submitted to the EMBL Data Library, March 1995
#accession       553198
##molecule_type DNA
#residues        1-212
#cross-references EMBL:X85285; NID:g736099; PID:g736100
#experimental_source isolate patient Ferracuti-2 90
GENETICS
#gene            C
CLASSIFICATION   #superfamily hepatitis B virus core antigen
KEYWORDS          alternative initiators; core protein
FEATURE
1-29              #domain signal sequence #status predicted #label SIG\
30-118            #product core antigen #status predicted #label CAG\
179-212           #domain carboxyl-terminal propeptide #link EAG #status
                    predicted #label ECP
SUMMARY          #length 212 #molecular-weight 24232 #checksum 593

```

```

REFERENCE      553112
#authors      Lai, M.E.; Mazzioleni, A.P.; Porru, A.; Balestrieri, A.
#submission   Submitted to the EMBL Data Library, March 1995
#accession    S53223
#molecule_1  DNA
#molecule_2  1-212 #label LAI
#residues     #cross-references EMBL:X85295; NID:g736134; PID:g726136
#experimental_source isolate patient Chighlone-1/85

GENETICS
#gene          C
CLASSIFICATION #superfamily hepatitis B virus core antigen
KEYWORDS        alternative initiators; core protein
FEATURE
1-29            #domain signal sequence #status predicted #label SIG\
30-212          #product core antigen #status predicted #label CAG\
30-178          #product e antigen #status predicted #label EAG\
179-212        #domain carboxyl-terminal propeptide #link EAG #status
                predicted #label Ecp
SUMMARY         #length 212 #molecular-weight 24364 #checksum 1123

Db      29 GMDIDPYKEFGATVELSLFLPSDFPSVRDLDDASALYRELLESPEHCSPHTALROAI 88
Oy      120 SMDIDPYKEFGATVELSLFLPSDFPSVRDLDDASALYRELLESPEHCSPHTALROAI 179
Db      89 LCMGDLMSLATWGVNLEBDPISRDLYSVYVNTNMGKFEROLMFEHISCLTGRETVIEYL 148
Oy      180 LCMGELMLTLATWGVNLEBDPASRDLYSVYVNTNMGKFEROLMFEHISCLTGRETVIEYL 239
Db      149 VSFQWITPPAIRPPNPAPILSTLPETTVVRRKGSPPRRKTPSPRRKRSQSPRRRRSSQR 208
Oy      240 VSFQWITPPAIRPPNPAPILSTLPETTVVRRKGSPPRRKTPSPRRKRSQSPRRRRSSQR 299
Db      209 ESOC 212
Oy      300 ESOC 303

```

```

RESULT      14
ENTRY
TITLE
ALTERNATE_NAMES
CONTAINS
ORGANISM
VARIETY
DATE
ACCESSIONS
REFERENCE
AUTHORS
SUBMISSION
ACCESSION
#molecule_type DNA
#residues 1-212 ##label IAI
#cross-references EMBL:X85316; NID:G9736208; PDB:G756210
#experimental_source isolate patient patient Giordo 84
GENETICS

```

ACCESSIONS

Query Match

60.48; Score 1366; DB 2; Length 212;

Best Local Similarity 98.9%; Pred. No. 6,45e-201;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 88
QY 120 SMDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 179
Db 89 LCMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFIISCLTFGRETIVIEL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFIISCLTFGRETIVIEL 239
Db 149 VSGVWIRTPPAYRPPNAPILITLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 240 VSGVWIRTPPAYRPPNAPILITLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 299
Db 209 ESOC 212
QY 300 ESOC 303

RESULT 15
ENTRY S53169 #type complete
TITLE core antigen - hepatitis B virus (isolate patient Muresu '89)
ALTERNATE_NAMES HBC antigen
CONTAINS core antigen
ORGANISM #formal_name hepatitis B virus, HBV
#isolate patient Muresu '89
#isolate patient Muresu '89
#sequence_revision 03-Aug-1995 #text_change 08-Sep-1997
DATE 08-Sep-1997

ACCESSIONS S53169
REFERENCE S53112
#authors Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
#submision submitted to the EMBL Data Library, March 1995
#accession S53169
#molecule_type DNA

GENETICS
#gene
CLASSIFICATION C
#superfamily hepatitis B virus core antigen
KEYWORDS core protein
SUMMARY #length 183 #molecular-weight 21088 #checksum 1849

Query Match 60.3%; Score 1364; DB 2; Length 183;
Best Local Similarity 98.4%; Pred. No. 1.41e-200;
Matches 180; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 60
QY 121 MDIDPKYKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 180
Db 61 CMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFIISCLTFGRETIVIEL 120
QY 181 CMGELMTLATWGVNLEDPASRDLVSVYNTNMGKFRQLMFIISCLTFGRETIVIEL 240
Db 121 SFGVWIRTPPAYRPPNAPILITLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
QY 241 SFGVWIRTPPAYRPPNAPILITLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 300
Db 181 SOC 183
QY 301 SOC 303

Search completed: Thu Dec 16 13:37:00 1999
Job time : 76 secs.

Matches 183: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALQAIL 60
  |||
Qy 121 MDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALQAIL 180
Db 61 CMGELMTLATWGVNLEDPASRDLYSVYNTNMGLKFRQLMFHISCLTFGRETVEIYLV 120
  |||
Qy 181 CMGELMTLATWGVNLEDPASRDLYSVYNTNMGLKFRQLMFHISCLTFGRETVEIYLV 240
Db 121 SEGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSRR 180
  |||
Qy 241 SEGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSRR 300
Db 181 SOC 183
  |||
Qy 301 SOC 303

RESULT 2
ID CORA_HPBVA STANDARD: PRT: 211 AA.
AC P24023:
DT 01-MAR-1992 (REL. 21, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (STRAIN ALPHA1).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90266476.
RA TONG S., LI J., VITVIRSKI L., TREPO C.;
RT "Active hepatitis B virus replication in the presence of anti-HBe is
associated with viral variants containing an inactive pre-C region.";
RL VIROLOGY 176:596-603(1990).
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CC -----
DR EMBL; M32138; G495034; ALT_SEQ.
DR PIR; A34773; NKVLA1.
DR PFAM; PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 183 190
FT REPEAT 198 206
SQ SEQUENCE 211 AA; 24208 MW; 0924CE5E CRC32;
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Query Match 60.0%; Score 1358; DB 1; Length 211;
Best Local Similarity 95.2%; Pred. No. 7.55e-231;
Matches 179: Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db 24 LGWLMDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 83
  |||
Qy 116 LGWLMDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTAL 175
Db 84 RQAILCWGDLITLSTWGVNLEDPTSRLVSVYNTNMGLKFRQLMFHISCLTFGRETVEIYLV 143
  |||
Qy 176 RQAILCWGDLITLSTWGVNLEDPTSRLVSVYNTNMGLKFRQLMFHISCLTFGRETVEIYLV 245
Db 144 IEVLVSGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSRR 203
  |||
Qy 236 IEVLVSGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSRR 295
Db 204 TQSRRESOC 211
  |||
Qy 296 TQSRRESOC 303
```

RESULT 3
ID CORA_HPBVZ STANDARD: PRT: 183 AA.
AC P03147;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW').
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81012115.
RA PASER M., GOTO T., GILBERT W., ZINK B., SCHALLER H., MCKAY P.,
RA LEADBETTER G., MURRAY K.;
RT "Hepatitis B virus genes and their expression in E. coli.";
RL NATURE 282:575-579(1979).

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CC -----
DR EMBL; J02202; G329638; -.
DR EMBL; A08967; G411874; -.
DR PIR; B93217; NKVLA2.
DR PFAM; PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21042 MW; 6EA6B674 CRC32;
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Query Match 59.6%; Score 1349; DB 1; Length 183;
Best Local Similarity 96.7%; Pred. No. 4.36e-229;
Matches 177: Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALQAIL 60
  |||
Qy 121 MDIDPKKFGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALQAIL 180
Db 61 CMGELMTLATWGVNLEDPASRDLYSVYNTNMGLKFRQLMFHISCLTFGRETVEIYLV 120
  |||
Qy 181 CMGELMTLATWGVNLEDPASRDLYSVYNTNMGLKFRQLMFHISCLTFGRETVEIYLV 240
Db 121 SEGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSRR 180
  |||
Qy 241 SEGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSOSRR 300
Db 181 SOC 183
  |||
Qy 301 SOC 303

RESULT 4
ID CORA_HPBVO STANDARD: PRT: 183 AA.
AC P17392:
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN OKINAWA/PODW282).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASIROSEMIGUNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
comparison of surface antigen subtypes.";
```

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RL J. GEN. VIROL. 69:2575-2583(1988).
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CC -----
CC
DR EMBL; D00330; -; NOT_ANNOTATED_CDS.
DR PIR; B28925; NKVLJ2.
DR PFAM; PF00906; Hepatitis_core; 1.
DR CORE_PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA; 21081 MW; 115B9E3 CRC32;
Query Match 59.0%; Score 1336; DB 1; Length 183;
Best Local Similarity 96.2%; Pred. No. 1,52e-226;
Matches 176; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db 1 MDIDYKEFGASVLELSELPDSDFPSVVDLDTASALYREALSESPHHTALRQAIL 60
QY 121 MDIDYKEFGATVELSLFLPSDFPSVVDLDTASALYREALSESPHHTALRQAIL 180
Db 61 CWGELMNLATWGSLEDPASRELVSIVYNNMGKIRQLMLFHISCLTFGRETILEYV 120
QY 181 CWGELMNLATWAGVLEDPASRDVLVSIVYNNMGKIRQLMLFHISCLTFGRETILEYV 240
Db 121 SFGVIRTPPARPPAPNADILSTLPETTVYRRGRSPRRTPSPRRRSOSPRRRSOSRE 180
QY 241 SFGVIRTPPARPPAPNAILSTLPETTVYRRGRSPRRTPSPRRRSOSPRRRSOSRE 300
Db 181 SQC 183
QY 301 SQC 303
RESULT 5
ID CORA_HPBV4 STANDARD; PRT: 183 AA.
AC P03150; P03151;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADR), HEPATITIS B VIRUS (SUBTYPE ADR4),
OS AND HEPATITIS B VIRUS (SUBTYPE ADM / STRAIN INOONSIA/P10M420).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ADR:
RC MEDLINE; 83168919.
RA ONO Y., ODA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;
RT "The complete nucleotide sequences of the cloned hepatitis B virus
RT DNA: subtype adr and adm."
RL NUCLEIC ACIDS RES. 11:1747-1757(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ADR4:
RC MEDLINE; 83246570.
RA FUJIYAMA A., MIYANOHARA A., NOZAKI C., YONEYAMA T., OTOMO N.,
RA MATSUBARA K.;
RT "Cloning and structural analyses of hepatitis B virus DNAs, subtype
RT adr."
RL NUCLEIC ACIDS RES. 11:4601-4610(1983).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ADM:
RC MEDLINE; 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAMA H., SASTROSOEMWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;

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RT      "Typing hepatitis B virus by homology in nucleotide sequence:
RT      Comparison of surface antigen subtypes.";
RL      J. GEN. VIROL. 69:2575-2583(1988).
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CC      -----
DR      EMBL: V00867; -. NOT_ANNOTATED_CDS.
DR      EMBL: X01587; G59407; -. NOT_ANNOTATED_CDS.
DR      EMBL: D00331; -. NOT_ANNOTATED_CDS.
DR      PIR: A93480; NKVL45.
DR      PIR: B93460; NKVL44.
DR      PIR: C28925; NKVLJ3.
DR      PIR: PF00906; Hepatitis_core; 1.
KW      CORE PROTEIN; REPEAT.
FT      REPEAT 162 169
FT      REPEAT 170 177
SQ      SEQUENCE 183 AA; 21095 MW; D2E185B9 CRC32;
Query Match 58.9%; Score 1334; DB 1; Length 183;
Best local similarity 95.6%; Pred. No.3,75e-226;
Matches 175; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Db 1 MDIDYKEFGASVELLSFLPSDFPFSIRDLDTASALYREALESPSCPHHTALRAAIL 60
Qy 121 MDIDYKEFGATVELLSLPSDFPFSVADLDLTASALYREALESPSCPHHTALRAAIL 180
Db 61 CWGELMNTATWGSLEDPASRELVSYSVNNMGKITQLMFHISCLTFGEYILEYV 120
Qy 181 CWGELMNTATWGSLEDPASRELVSYSVNNMGKITQLMFHISCLTFGEYILEYV 240
Db 121 SFGVWIRTPAARPNAPNAILSLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 180
Qy 241 SFGVWIRTPAARPNAPNAILSLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 300
Db 181 SQC 183
Qy 301 SQC 303
RESULT 6
ID ID CORA_HBVJ STANDARD; PRT; 183 AA.
AC P17391;
DT 01-AUG-1990 (REL. 15, CREATED)
DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN JAPAN/PJW233).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89010694.
RA OKAMOTO H., TSUDA F., SAKUGAWA H., SASTROSEWIGNO R.I., IMAI M.,
RA MIYAKAWA Y., MAYUMI M.;
RT "Typing hepatitis B virus by homology in nucleotide sequence:
RT comparison of surface antigen subtypes.";
RL J. GEN. VIROL. 69:2575-2583(1988).
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CC -----
DR EMBL: D00329; -. NOT_ANNOTATED_CDS.
DR PIR: A28925; NKVLJ1.

```

DR PFAM: PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 162 169
FT REPEAT 170 177
SQ SEQUENCE 183 AA: 21224 MW: F6B348B6 CRC32:

Query Match 58.4%; Score 1322; DB 1; Length 183;
Best Local Similarity 96.2%; Pred. No. 8,34e-224;
Matches 176; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
121 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 180
Db 61 CMCGLMTLATWGNLDEDPASRDLYVNYVTNGLKIRQLMWHISCLTFGRRTVEIY 120
181 CMCGLMTLATWGNLDEDPASRDLYVNYVTNGLKIRQLMWHISCLTFGRRTVEIY 240
Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 180
241 SFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 300
Db 181 SOC 183
111
QY 301 SOC 303

RESULT 7
ID CORA_HPBVT STANDARD: PRT; 185 AA.

AC P03149;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1989 (REL. 12, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.

GN C.
OS HEPATITIS B VIRUS (SUBTYPE ADW).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RX MEDLINE: 83168919.

RA ONO Y., ONDA H., SASADA R., IGARASHI K., SUGINO Y., NISHIOKA K.;

RT "The complete nucleotide sequences of the cloned hepatitis B virus
DNA: subtype adr and adv.";

RL NUCLEIC ACIDS RES. 11:1747-1757(1983).

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CC EMBL: V00866; -; NOT_ANNOTATED_CDS.

DR PIR: C93460; NKVLN6.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN; REPEAT.

FT REPEAT 164 171

FT REPEAT 172 179

SQ SEQUENCE 185 AA: 21394 MW: 791E0381 CRC32:

Query Match 58.4%; Score 1321; DB 1; Length 185;
Best Local Similarity 96.2%; Pred. No. 1,31e-223;
Matches 178; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 60
121 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 180
Db 61 CMCGLMTLATWGNLDEDPASRDLYVNYVTNGLKIRQLMWHISCLTFGRRTVEIY 120
181 CMCGLMTLATWGNLDEDPASRDLYVNYVTNGLKIRQLMWHISCLTFGRRTVEIY 240

Db 121 SFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 180
241 SFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 298
Db 181 RESOC 185
11111
QY 299 RESOC 303

RESULT 8
ID CORA_HPBVT STANDARD: PRT; 195 AA.

AC P29178;
DT 01-DEC-1992 (REL. 24, CREATED)
DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.

GN C.

OS HEPATITIS B VIRUS (SUBTYPE ADW2 VARIANT SF).

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RX MEDLINE: 90169850.

RA BHAT R.A., ULRICH P.P., VYAS G.N.;

RT "Molecular characterization of a new variant of hepatitis B virus in
a persistently infected homosexual man.";

RL HEPATOLOGY 11:271-276(1990).

DR PIR: A37182; NKVLH3.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN; REPEAT.

FT REPEAT 174 181

FT REPEAT 182 189

SQ SEQUENCE 195 AA: 22461 MW: AE3DB5F3 CRC32:

Query Match 58.1%; Score 1314; DB 1; Length 195;
Best Local Similarity 93.5%; Pred. No. 3,06e-222;
Matches 173; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Db 11 FGLIDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 70

QY 119 LMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALQAIL 178

Db 71 IICWELMTLATWGNLDEDPASRDLYVNYVTNGLKIRQLMWHISCLTFGRRTVEIY 130

QY 179 IICWELMTLATWGNLDEDPASRDLYVNYVTNGLKIRQLMWHISCLTFGRRTVEIY 238

Db 131 IVSFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 190

QY 239 IVSFGWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSR 298

Db 191 RESOC 195

QY 299 RESOC 303

RESULT 9
ID CORA_HPBVT STANDARD: PRT; 212 AA.

AC Q05495;

DT 01-NOV-1995 (REL. 32, CREATED)

DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

GN C.

OS HEPATITIS B VIRUS (SUBTYPE ADW4 / STRAIN BRAZIL / ISOLATE W4B).

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

RN [1]
RX MEDLINE: 93346970.

RA NAUDANN H., SCHAEFER S., YOSHIDA C.F.T., GASPAR A.M.C., REPP R.,

RA GERLICH W.H.;

RT "Identification of a new hepatitis B virus (HBV) genotype from Brazil
that expresses HBV surface antigen subtype adw4.";

RL J. GEN. VIROL. 74:1627-1632(1993).

CC -----

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DR EMBL: X69798; G59423; -

KW CORE PROTEIN: REPEAT. 1.

FT DOMAIN 178 204 ARG-RICH.

FT REPEAT 184 203 3 X 5 AA REPEATS OF S-P-R-R-R.

FT REPEAT 184 188 1.

FT REPEAT 191 195 2.

FT REPEAT 199 203 3.

SO SEQUENCE 212 AA; 24234 MM; BCCDF263 CRC32;

Query Match 58.0%; Score 1313; DB 1; Length 212;

Best Local Similarity 92.9%; Pred. No. 4,79e-222;

Matches 171; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

DB 29 GMDIDPKFEGATVELLSPLSPDFPSVVDLDTASALYREALSEPHCSPHHTALROAI 88

OY 120 SMDIDPKFEGATVELLSPLSPDFPSVVDLDTASALYREALSEPHCSPHHTALROAI 179

DB 89 LCMGELMTLASVGNLLEDPASRDVLYVNTNMGKIRQLMFHISCLTFGRETLYEYL 148

OY 180 LCMGELMTLATVGNLLEDPASRDVLYVNTNMGKIRQLMFHISCLTFGRETLYEYL 239

DB 149 VSEGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSP 208

OY 240 VSEGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSP 299

DB 209 ASOC 212

OY 300 ESOC 303

RESULT 10

ID CORA_HPBVL STANDARD; PRT: 183 AA.

AC P12901; 01-OCT-1989 (REL. 12, CREATED)

DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)

DT 01-APR-1990 (REL. 14, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

C. HEPATITIS B VIRUS (STRAIN LSH / CHIMPANZEE ISOLATE).

OS VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

OC [1]

NC SEQUENCE FROM N.A.

RP MEDLINE: 88258473.

RA VAUDIN M., WOJSTENHOLME A.J., TSIOUAE K.N., ZUCKERMAN A.J.,

RT HARRISON T.J.;

RT "The complete nucleotide sequence of the genome of a hepatitis B

virus isolated from a naturally infected chimpanzee.";

RL J. GEN. VIROL. 69:1383-1389(1988).

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DR EMBL: D00220; D100603; -

DR PIR: A28885; NKVLCF.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN: REPEAT.

FT REPEAT 162 169

FT REPEAT 170 177

SO SEQUENCE 183 AA; 20999 MM; 1AF57C9 CRC32;

Query Match 57.8%; Score 1308; DB 1; Length 183;

Best Local Similarity 94.5%; Pred. No. 4,55e-221;

Matches 173; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

DB 1 MDIDPKFEGATVELLSPLSPDFPSVVDLDTASALYREALSEPHCSPHHTALROAI 60

OY 121 MDIDPKFEGATVELLSPLSPDFPSVVDLDTASALYREALSEPHCSPHHTALROAI 180

DB 61 CWMGELMTLASVGNLLEDPASRDVLYVNTNMGKIRQLMFHISCLTFGRETLYEYL 120

OY 181 CWMGELMTLATVGNLLEDPASRDVLYVNTNMGKIRQLMFHISCLTFGRETLYEYL 240

DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSPA 180

OY 241 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSPRE 300

DB 181 SOC 183

OY 301 SOC 303

RESULT 11

ID CORA_HPBV2 STANDARD; PRT: 185 AA.

AC P03148; 21-JUL-1986 (REL. 01, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

C. HEPATITIS B VIRUS (SUBTYPE ADW2).

OS VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.

OC [1]

NC SEQUENCE FROM N.A.

RP VALENZUELA P., QUIROGA M., ZAIDIYAR J., GRAY P., RUTTER W.J.;

RL (IN) FIELD B.N., JAEINISCH R., FOX C.F. (EDS.);

RL ANIMAL VIRUS GENETICS, PP. 57-70, ACADEMIC PRESS, NEW YORK (1980).

DR PIR: A94409; NKVLA3.

DR PFAM: PF00906; Hepatitis_core; 1.

KW CORE PROTEIN: REPEAT.

FT REPEAT 164 171

FT REPEAT 172 179

SO SEQUENCE 185 AA; E2EA3360 CRC32;

Query Match 57.7%; Score 1305; DB 1; Length 185;

Best Local Similarity 95.7%; Pred. No. 1,76e-220;

Matches 177; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

DB 1 MDIDPKFEGATVELLSPLSPDFPSVVDLDTASALYREALSEPHCSPHHTALROAI 60

OY 121 MDIDPKFEGATVELLSPLSPDFPSVVDLDTASALYREALSEPHCSPHHTALROAI 180

DB 61 CWMGELMTLATVGNLLEDPASRDVLYVNTNMGKIRQLMFHISCLTFGRETLYEYL 120

OY 181 CWMGELMTLATVGNLLEDPASRDVLYVNTNMGKIRQLMFHISCLTFGRETLYEYL 240

DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSP 180

OY 241 SFGVWIRTPPAYRPPNAPILSTLPETTVARRGRSPRRRTSPRRRSQSPRRRSQSP 298

DB 181 RESOC 185

OY 299 RESOC 303

RESULT 12

ID CORA_HPBV9 STANDARD; PRT: 214 AA.

AC P17099; 01-AUG-1990 (REL. 15, CREATED)

DT 01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)

DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)

DE CORE ANTIGEN.

C.

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OS HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN 991).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA KOCHHEL H.G., SCHUELER A., LOTTMANN S., THOMSEN R.;
RL SUBMITTED (FEB-1990) TO EMBL/GENBANK/DBJ DATA BANKS.
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DR EMBL; X51970; G60433; -
DR PIR; S10381; NKVLKS.
DR PFAM; PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 193 200
FT REPEAT 201 208
SQ SEQUENCE 214 AA; 24722 MW; 786CD048 CRC32;

Query Match 57.6%; Score 1304; DB 1; Length 214;
Best Local Similarity 95.2%; Pred. No. 2,75e-220;
Matches 177; Conservative 5; Mismatches 2; Indels 2; Gaps 1;

DB 29 GMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 88.
QY 120 SMDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 179
DB 89 LCMGELMTLATWGVNLEDPASRDLYVYVNTNMGKRLQMLFISLTFTGRETIVLEYL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYVYVNTNMGKRLQMLFISLTFTGRETIVLEYL 239
DB 149 VSGFWITPPAYRPPNAPILSTLPETTVARRRGSRPRTTSPRRRSQSPRRRSQ 208
QY 240 VSGFWITPPAYRPPNAPILSTLPETTVARRRGSRPRTTSPRRRSQSPRRRSQ 297
DB 209 SRESOC 214
QY 298 SRESOC 303

RESULT 13
ID CORA_HV1 STANDARD; PRT; 188 AA.
AC P03152;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS WOODCHUCK HEPATITIS VIRUS 1 (WHV 1),
OS WOODCHUCK HEPATITIS VIRUS 7 (WHV 7),
OS WOODCHUCK HEPATITIS VIRUS 59 (WHV 59), AND
OS WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE) (WHV 8).
OC WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE) (WHV 8).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA SPECIES-WOODCHUCK HEPATITIS VIRUS 1;
RX MEDLINE; 82216969.
RA GALIBERT F., CHEN T.N., MANDART E.;
RT "Nucleotide sequence of a cloned woodchuck hepatitis virus genome:
RT comparison with the hepatitis B virus sequence.";
RL J. VIROL. 41:51-65(1982).

RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES-WOODCHUCK HEPATITIS VIRUS 7, AND WOODCHUCK HEPATITIS VIRUS 59;
RX MEDLINE; 88101359.
RA COHEN J.I., MILLER R.H., ROSENBLUM B., DENNISTON K., GERIN J.L.,
RA PUCCELL R.H.;
RT "Sequence comparison of woodchuck hepatitis virus replicative forms
RT shows conservation of the genome.";

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RL VIROLOGY 162:12-20(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-WOODCHUCK HEPATITIS VIRUS 8 (INFECTIOUS CLONE);
RX MEDLINE; 89184524.
RA GIRONES R., CORE P.J., HORNBUCKLE W.E., TENNANT B.C., GERIN J.L.,
RA PUCCELL R.H., MILLER R.H.;
RT "Complete nucleotide sequence of a molecular clone of woodchuck
RT hepatitis virus that is infectious in the natural host.";
RL PROC. NATL. ACADE. SCI. U.S.A. 86:1846-1849(1989).
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DR EMBL; J02442; G336129; -
DR EMBL; M18752; G336140; -
DR EMBL; M19183; G336145; -
DR EMBL; J04514; G336149; -
DR PIR; A03713; NKVLC.
DR PIR; C32397; NKVLC.
DR PIR; C32397; NKVLC4.
DR PIR; C32397; NKVLC3.
DR PFAM; PF00906; Hepatitis_core; 1.
KW CORE PROTEIN; REPEAT.
FT REPEAT 167 174
FT REPEAT 175 182
SQ SEQUENCE 188 AA; 21693 MW; A667DB27 CRC32;

Query Match 41.4%; Score 938; DB 1; Length 188;
Best Local Similarity 67.0%; Pred. No. 3.26e-149;
Matches 126; Conservative 25; Mismatches 32; Indels 5; Gaps 1;

DB 1 MDIDPYKEFGSSVQLNLFPLDFFPDINALVDATATLYEELTGREHCSPHHTALROAI 60
QY 121 MDIDPYKEFGATVLLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTALROAI 180
DB 61 CWDLTFLIAMSNSINSEQRTIVVHNDTWGLKRYOSTMFLHSLTGTOHVEFLY 120
QY 181 CWDLTFLIAMSNSINSEQRTIVVHNDTWGLKRYOSTMFLHSLTGTOHVEFLY 240
DB 121 SFGWITPPAYRPPNAPILSTLPETTVARRRGSRPRTTSPRRRSQSPRRRR 180
QY 241 SFGWITPPAYRPPNAPILSTLPETTVARRRGSRPRTTSPRRRSQSPRRRR 295
DB 181 SQSPSANC 188
QY 296 SQSPSANC 303

RESULT 14
ID CORA_HPGS STANDARD; PRT; 217 AA.
AC P03153;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN.
GN C.
OS GROUND SQUIRREL HEPATITIS VIRUS (GSV).
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84267998.
RA SEEGER C., GANEM D., VARMUS H.E.;
RT "Nucleotide sequence of an infectious molecularly cloned genome of
RT ground squirrel hepatitis virus.";
RL J. VIROL. 51:367-375(1984).
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Dd      1 MDIDYKEFGSSYDILNMFLEIDPEFPDNLAVDTATAYALIEELGRKCSPHHAIKRALV 60
Qy      121 MDIDPYKEFGATVELLSFLSPDFSPRDLIDTASALYIRALSPESPCSHHAIKRAIL 160
Dd      61 CMDELTKLIAMSSNITSEQVRTIIYNHVNDWGLKVKRQSLMFHLSCLTFEGQHTVOEFLV 120
Qy      181 CMGSELMTLATWGVNLEBDPASRDVLVSXVNTNMGLKFROLLMEHISCLTFGRETVIEYLV 240
Dd      121 SFVVMIRTPAPYRPPNAPILSTLPEHVIRGCGAKARSRPRRRTPSPRRRRSSPPRRRS 180
Qy      241 SFEGWIRTPAPYRPPNAPILSTLPETVRR--RG-RSPRRRTPSPRRRRSSPPRRRS 296
Dd      181 QSPSANC 187
Qy      297 QSRSEQC 303

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Search completed: Thu Dec 16 13:37:51 1999
Job time : 34 secs.

Query Match 60.88; Score 1375; DB 14; Length 212;
Best Local Similarity 99.5%; Pred. No. 3.10e-221;
Matches 183; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 88
QY 120 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 179
DB 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 239
DB 149 VSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSOSPRRRRSOSR 208
QY 240 VSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSOSPRRRRSOSR 299
DB 209 ESOC 212
QY 300 ESOC 303

RESULT 2
ID 089437 PRELIMINARY; PRT; 183 AA.

AC 089437:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (CASTAA 2).
GN CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RC SEQUENCE FROM N.A.
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN-AYW;
RC KARAYIANNIS P.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RC SEQUENCE FROM N.A.
RA STRAIN-AYW;
RC KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85289; G736113; -;
DR EMBL: X80925; E198085; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 183 AA; 21102 MW; 0C504D47 CRC32;

Query Match 60.7%; Score 1373; DB 14; Length 183;
Best Local Similarity 99.5%; Pred. No. 7.27e-221;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 1 MDDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 60
QY 121 MDDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 180
DB 61 CMEGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 120
QY 181 CMEGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 240
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSOSPRRRRSOSR 180
QY 241 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSOSPRRRRSOSR 300
DB 181 SOC 183
QY 301 SOC 303

RESULT 3

ID 068008 PRELIMINARY; PRT; 183 AA.

AC 068008:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (FERRACUT 1).
GN CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RC SEQUENCE FROM N.A.
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85284; G736098; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 183 AA; 21102 MW; BB9AFB3 CRC32;

Query Match 60.7%; Score 1373; DB 14; Length 183;
Best Local Similarity 99.5%; Pred. No. 7.27e-221;
Matches 182; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 1 MDDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 60
QY 121 MDDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 180
DB 61 CMEGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 120
QY 181 CMEGLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 240
DB 121 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSOSPRRRRSOSR 180
QY 241 SFGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSOSPRRRRSOSR 300
DB 181 SOC 183
QY 301 SOC 303

RESULT 4
ID 068020 PRELIMINARY; PRT; 212 AA.

AC 068020:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN-PATIENT CASTAG-1'85;
RA LAI M.E., MAZZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85281; G736119; -;
DR PFAM: PF00906; Hepatitis_core; 1.
SQ SEQUENCE 212 AA; 24336 MW; E0E4C243 CRC32;

Query Match 60.7%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 4.75e-221;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 29 GMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 88
QY 120 SMDIDPKKEGATVELLSFLPSDFPSVRDLDTASALYREALSEPHCSPHHTALROAI 179
DB 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 239
DB 149 VSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSOSPRRRRSOSR 208
QY 240 VSGVWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRTPSPRRRSOSPRRRRSOSR 299

Db 209 ESOC 212
|||
QY 300 ESOC 303

RESULT 5
ID 089597 PRELIMINARY: PRT: 212 AA.
AC 089597:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HBAG.
OS HEPATITIS B VIRUS.
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUB-TYPE AYW;
RX MEDLINE: 94079539.
RA PREISLER-ADAMS S., SCHLAYER M.J., PETERS T., HETTLER F., GEROK W.,
RA RASENACK J.;
RT "Sequence analysis of hepatitis B virus DNA in immunologically
negative infection."
RL ARCH. VIROL. 133:385-396(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-AYW;
RA KARAYIANNIS P.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X72702; G288930; -;
DR EMBL: X80925; E198084; -;
DR PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24336 MW; 575D20BF CRC32;

Query Match 60.7%; Score 1374; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 4,75e-221;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKYKFGATVELLSFLPSDFPSVRLDLDTRASALYREALSPHCSPHHTALROAI 88
:|||||
QY 120 SMDIDPKYKFGATVELLSFLPSDFPSVRLDLDTRASALYREALSPHCSPHHTALROAI 179

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLMFIISCLTGTGRETIVIEL 148
|||||
QY 180 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLMFIISCLTGTGRETIVIEL 239

Db 149 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSOSR 208
:|||||
QY 240 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSOSR 299

Db 209 ESOC 212
|||
QY 300 ESOC 303

RESULT 6
ID 067876 PRELIMINARY: PRT: 212 AA.
AC 067876:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE C/C ORF.
OS HEPATITIS B VIRUS.
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CT, HBV SUBTYPE AYW;
RA LAI M.E., MAZZOLENI A.P., BALESTRIERI A., MELIS A., PORRU A.;

RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65258; G59436; -;
DR PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24348 MW; 6ED741BE CRC32;

Query Match 60.7%; Score 1373; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 7,27e-221;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKYKFGATVELLSFLPSDFPSVRLDLDTRASALYREALSPHCSPHHTALROAI 88
:|||||
QY 120 SMDIDPKYKFGATVELLSFLPSDFPSVRLDLDTRASALYREALSPHCSPHHTALROAI 179

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLMFIISCLTGTGRETIVIEL 148
|||||
QY 180 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLMFIISCLTGTGRETIVIEL 239

Db 149 VAFGWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSOSR 208
:|||||
QY 240 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSOSR 299

Db 209 ESOC 212
|||
QY 300 ESOC 303

RESULT 7
ID 011884 PRELIMINARY: PRT: 212 AA.
AC 011884:
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE CORE ANTIGEN PRECURSOR.
OS HEPATITIS B VIRUS.
OC VIRUSES: RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RA RAO B.S., CASEY J.L., RINAUDO J.S., KORBA B.E.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U95551; G2182120; -;
DR PFAM: PF00906; Hepatitis_core: 1.
SQ SEQUENCE 212 AA; 24360 MW; 73AC92DB CRC32;

Query Match 60.6%; Score 1372; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 1,11e-220;
Matches 182; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPKYKFGATVELLSFLPSDFPSVRLDLDTRASALYREALSPHCSPHHTALROAI 88
:|||||
QY 120 SMDIDPKYKFGATVELLSFLPSDFPSVRLDLDTRASALYREALSPHCSPHHTALROAI 179

Db 89 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLMFIISCLTGTGRETIVIEL 148
|||||
QY 180 LCMGELMTLATWGVNLEDPASRDVSVYNTNMGKFRQLMFIISCLTGTGRETIVIEL 239

Db 149 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSOSR 208
:|||||
QY 240 VSGFWIRTPPAYRPPNAPILSTLPETTVVRRGRSPRRRTSPRRRSQSPRRRSOSR 299

Db 209 EPQC 212
|||
QY 300 ESOC 303

RESULT 8
ID 068066 PRELIMINARY: PRT: 183 AA.
AC 068066:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE X, PREC AND C GENES (LICHERI 2).
OS HEPATITIS B VIRUS.

OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LICHERI-2/87;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85314; G736204; -
PRAM: PF00906; Hepatitis_core: 1
SQ SEQUENCE 183 AA; 21102 MW; 6F38AA3B CRC32;
Query Match 60.5%; Score 1370; DB 14; Length 183;
Best Local Similarity 98.4%; Pred. No. 2.60e-220;
Matches 180; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Db 1 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHNTALRQAI 60
QY 121 MDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHNTALRQAI 180
Db 61 CWGDLMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 120
QY 181 CWGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 240
Db 121 SFGWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 180
QY 241 SFGWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 300
Db 181 SQC 183
QY 301 SQC 303
RESULT 9 PRELIMINARY; PRT: 212 AA.
ID 068068 AC 068068;
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN HEPATITIS B VIRUS.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT LICHERI-3/90;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85315; G736207; -
PRAM: PF00906; Hepatitis_core: 1
SQ SEQUENCE 212 AA; 24366 MW; AB227A9B CRC32;
Query Match 60.5%; Score 1370; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 2.60e-220;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 29 GMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHNTALRQAI 88
QY 120 SMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHNTALRQAI 179
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 239
Db 149 VSGWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 240 VSGWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 299
Db 209 ESQC 212
QY 300 ESQC 303
RESULT 10 PRELIMINARY; PRT: 212 AA.
ID 068025

AC 068025;
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CASTAG/3;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X85293; G736126; -
PRAM: PF00906; Hepatitis_core: 1
SQ SEQUENCE 212 AA; 24363 MW; A6A254DF CRC32;
Query Match 60.5%; Score 1370; DB 14; Length 212;
Best Local Similarity 98.9%; Pred. No. 2.60e-220;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 29 GMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHNTALRQAI 88
QY 120 SMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHNTALRQAI 179
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 239
Db 149 VSGWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 240 VSGWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 299
Db 209 ESQC 212
RESULT 11 PRELIMINARY; PRT: 212 AA.
ID 067872 AC 067872;
DT 01-NOV-1996 (TREMREL. 01, CREATED)
DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE PRE C/C ORF.
GN HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT C, HBSAG POSITIVE, HBV SUBTYPE AYW;
RA LAI M.E., MAZOLENI A.P., BALESTRIERI A., MELIS A., PORRU A.;
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: X65257; G59431; -
PRAM: PF00906; Hepatitis_core: 1
SQ SEQUENCE 212 AA; 24348 MW; A6BD9DA1 CRC32;
Query Match 60.5%; Score 1369; DB 14; Length 212;
Best Local Similarity 98.4%; Pred. No. 3.98e-220;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 29 GMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHNTALRQAI 88
QY 120 SMDIDPYKEGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHNTALRQAI 179
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKLFROLMFHISCLTFGRETVIEYL 239
Db 149 VSGWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 240 VSGWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 299
Db 209 ESQC 212

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QY 300 ESOC 303

RESULT 12
ID 067984 PRELIMINARY: PRT: 212 AA.
AC 067984:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT VITTORINA'92;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR PFAM: PF00906; Hepatitis core; 1.
SQ SEQUENCE 212 AA; 24322 MM; 83D9780B CRC32;

Query Match
Best Local Similarity 98.9%; Score 1369; DB 14; Length 212;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTLRQAI 88
QY 120 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTLRQAI 179
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTGFRETIVIEL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTGFRETIVIEL 239
Db 149 VSGVWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 240 VSGVWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 299
Db 209 ESOC 212
QY 300 ESOC 303

RESULT 13
ID 068032 PRELIMINARY: PRT: 212 AA.
AC 068032:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CHIGHINE-2'86;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR PFAM: PF00906; Hepatitis core; 1.
SQ SEQUENCE 212 AA; 24308 MM; 69D87B53 CRC32;

Query Match
Best Local Similarity 98.4%; Score 1369; DB 14; Length 212;
Matches 181; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTLRQAI 88
QY 120 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTLRQAI 179
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTGFRETIVIEL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTGFRETIVIEL 239
Db 149 VSGVWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 240 VSGVWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 299
Db 209 ESOC 212
QY 300 ESOC 303
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QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTGFRETIVIEL 239
Db 149 VSGVWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 240 VSGVWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 299
Db 209 ESOC 212
QY 300 ESOC 303

RESULT 14
ID 068010 PRELIMINARY: PRT: 212 AA.
AC 068010:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT FERRACUTI-2'90;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR PFAM: PF00906; Hepatitis core; 1.
SQ SEQUENCE 212 AA; 24292 MM; 04A4D12D CRC32;

Query Match
Best Local Similarity 98.4%; Score 1368; DB 14; Length 212;
Matches 181; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 29 GMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTLRQAI 88
QY 120 SMDIDPYKEFGATVELLSFLPSDFPSVRDLDTASALYREALSPHCSPHHTLRQAI 179
Db 89 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTGFRETIVIEL 148
QY 180 LCMGELMTLATWGVNLEDPASRDLYSVYNTNMGKRFOLMFHISCLTGFRETIVIEL 239
Db 149 VSGVWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 208
QY 240 VSGVWIRTPPAYRPNAPILSTLPETTVRRGRSPRRRTSPRRRSQSPRRRSQSR 299
Db 209 ESOC 212
QY 300 ESOC 303

RESULT 15
ID 068070 PRELIMINARY: PRT: 212 AA.
AC 068070:
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PRE-C/CORE.
GN PRE-C/CORE.
OS HEPATITIS B VIRUS.
OC VIRUSES; RETROID VIRUSES; HEPADNAVIRIDAE; ORTHOHEPADNAVIRUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT GIORDO'84;
RA LAI M.E., MAZOLENI A.P., PORRU A., BALESTRIERI A.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR PFAM: PF00906; Hepatitis core; 1.
SQ SEQUENCE 212 AA; 24376 MM; 80F52D0F CRC32;

Query Match
Best Local Similarity 98.4%; Score 1366; DB 14; Length 212;
Matches 182; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db      29 GMDIDPYKEFGATVELLSFLPSDFPSYRDLLDTASALYREALESPENHSPHHTALROAI 88
      : |||||
QY      120 SMDIDPYKEFGATVELLSFLPSDFPSYRDLLDTASALYREALESPENHSPHHTALROAI 179
      : |||||
Db      89 LCWGEIEMTLATWGVNLEDPAASRDIVSYVNTNMGKFRQLWFIHISCLTFGRETVEYL 148
      : |||||
QY      180 LCWGEIEMTLATWGVNLEDPAASRDIVSYVNTNMGKFRQLWFIHISCLTFGRETVEYL 239
      : |||||
Db      149 VSGVWIRTPPAYRPPNAPILTLLETIVRRGRSPRRRTPSPRRRSQSPRRRSQSR 208
      : |||||
QY      240 VSGVWIRTPPAYRPPNAPILTLLETIVRRGRSPRRRTPSPRRRSQSPRRRSQSR 299
      : |||||
Db      209 ESQC 212
      : |||||
QY      300 ESQC 303

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